

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MPearch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 18:57:00 1997; Maspar time 1002.71 Seconds

Tabular output not generated.

Title: >US-08-699-716A-1
Description: (1-1566) from US08699716A.seq
Perfect Score: 1566
N.A. Sequence: 1 ANGGGCGATCATCATCATCA.....ATGACACGTCTGTGTAATGA 1566
Comp: TACCGGTAGTACTAGTACTAGT.....TACTGTGACAGACCATTTACT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS

1:EST9 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99

Database:

EST-STS-TWO

100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109
110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
125:EST125 126:EST126 127:EST127 128:EST128 129:EST129
130:EST130 131:EST131 132:EST132 133:EST133 134:EST134
135:EST135 136:EST136 137:EST137 138:EST138 139:EST139
140:EST140 141:EST141 142:EST142 143:EST143 144:EST144
145:EST145 146:EST146 147:EST147 148:EST148 149:EST149
150:EST150 151:EST151 152:EST152 153:EST153 154:EST154
155:EST155 156:EST156 157:EST157 158:EST158 159:EST159
160:EST160 161:EST161 162:EST162 163:EST163 164:EST164
165:EST165 166:EST166 167:EST167 168:EST168 169:EST169
170:EST170 171:EST171 172:EST172 173:EST173 174:EST174

BEST AVAILABLE COPY

Database:

EST-STS-THREE

175:EST175 176:EST176 177:EST177 178:EST178 179:EST179
180:EST180 181:EST181 182:EST182 183:EST183 184:EST184
185:EST185 186:EST186 187:EST187 188:EST188 189:EST189
190:EST190 191:EST191 192:EST192 193:EST193
194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6
200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12
206:STS13 207:STS14 208:STS15 209:STS16 210:STS17
211:STS18 212:STS19 213:STS20 214:STS21 215:STS22
216:STS23 217:STS24 218:STS25 219:STS26
220:STS27 221:STS28 222:STS29 223:STS30 224:STS31
225:STS32 226:STS33 227:STS34 228:STS35 229:STS36
230:STS37 231:STS38 232:STS39 233:STS40 234:STS41
235:STS42 236:STS43 237:STS44 238:STS45
239:STS46 240:STS47 241:STS48 242:STS49
243:STS50 244:STS51 245:STS52 246:STS53
247:STS54 248:STS55 249:STS56 250:STS57
251:STS58

Statistics: Mean 11.349; Variance 2.120; scale 5.354

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	33	2.1	451	197	G09413	human STR CHLC.ATC1.P 3.12e-18
2	32	2.0	231	81	N43326	Y45910.r1 Homo sapie 1.07e-16
3	31	2.0	239	197	G08851	human STR CHLC.ATC3C1 3.44e-15
4	31	2.0	255	251	PCU64650	Parachartergus colobo 3.44e-15
5	31	2.0	255	205	PCU64650	Parachartergus colobo 3.44e-15
6	31	2.0	255	204	PCU64650	Parachartergus colobo 3.44e-15
7	31	2.0	256	196	G08117	human STR CHLC.ATC3E0 3.44e-15
8	31	2.0	298	203	HS8346TB5	human STR CHLC.ATC3E0 3.44e-15
9	32	2.0	314	197	G08591	human STR CHLC.ATC6.P 1.07e-16
10	31	2.0	377	197	G09253	human STR CHLC.ATC2F0 3.44e-15
11	31	2.0	514	19	ATTS1025	A. thaliana transcrib 3.44e-15
12	32	2.0	521	205	HDWUT7996	human STR UT7996 1.07e-16
13	32	2.0	521	204	HDWUT7996	human STR UT7996 1.07e-16
14	31	2.0	588	197	G09471	human STR CHLC.ATC5A0 3.44e-15
15	30	1.9	277	197	G09999	human STR CHLC.GC116B 1.04e-13
16	30	1.9	311	197	G10330	human STR CHLC.ATC7F0 1.04e-13
17	30	1.9	326	205	HDWUT8005B	human STR UT8005, 3' 1.04e-13
18	30	1.9	326	205	HDWUT8005B	human STR UT8005, 3' 1.04e-13
19	30	1.9	332	197	G09256	human STR CHLC.ATC3C1 1.04e-13
20	30	1.9	334	197	G10329	human STR CHLC.ATC6F1 1.04e-13
21	21	1.9	339	197	G09261	human STR CHLC.ATC2F0 1.04e-13
22	30	1.9	342	204	HDWUT7997	human STR UT7997 1.04e-13
23	30	1.9	342	205	HDWUT7997	human STR UT7997 1.04e-13
24	30	1.9	345	197	G09257	human STR CHLC.ATC2B1 1.04e-13
25	30	1.9	359	104	R23641	human STR CHLC.ATC2B1 1.04e-13
26	30	1.9	366	205	HDWUT1040	human STR UT1040 1.04e-13
27	30	1.9	366	205	HDWUT1040	human STR UT1040 1.04e-13
28	30	1.9	366	205	G08221	human STR CHLC.ATC3A0 1.04e-13
29	30	1.9	372	85	HSPD03455	H. sapiens EST sequenc 1.04e-13
30	30	1.9	372	222	HSPD03455	H. sapiens EST sequenc 1.04e-13
31	30	1.9	385	197	G08663	human STR CHLC.ATC2B1 1.04e-13
32	30	1.9	387	197	G09248	human STR CHLC.ATC2B1 1.04e-13
33	30	1.9	403	197	G09249	human STR CHLC.ATC2C0 1.04e-13
34	30	1.9	407	54	H85715	Y688906.r1 Homo sapie 1.04e-13
35	35	1.9	446	204	M78296	EST00444 Homo sapie 1.04e-13
36	30	1.9	446	204	HDWUT6615	human STR UT6615 1.04e-13
37	30	1.9	444	205	HDWUT6615	human STR UT6615 1.04e-13
38	30	1.9	521	140	R76963	human STR UT6615 1.04e-13
39	29	1.9	534	55	H91490	SYMFA007.r1 Homo sapie 2.97e-12
40	30	1.9	559	198	G15746	human STR CHLC.ATC5H0 1.04e-13
41	30	1.9	588	197	G09469	human STR CHLC.ATC4C0 1.04e-13
42	30	1.9	625	197	G09478	human STR CHLC.ATC4D0 1.04e-13
43	30	1.9	634	205	HDWUT6629	human STR UT6629 1.04e-13

ACCESSION U64650
NID 91495941
KEYWORDS STS.
SOURCE Parachartergus colobopteranus.
ORGANISM Parachartergus colobopteranus.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Parachartergus.
REFERENCE 1 (bases 1 to 255)
AUTHORS Strassmann, J.E., Solis, C.R., Barefield, K. and Queller, D.C.
TITLE Trinucleotide microsatellite loci in a swarm-founding neotropical wasp, Parachartergus colobopteranus and their usefulness in other social wasps
JOURNAL Mol. Ecol. 5 (3), 459-461 (1996)
MEDLINE 96266704
REFERENCE 2 (bases 1 to 255)
AUTHORS Strassmann, J.E., Hughes, C.R., Barefield, K., Solis, C.R. and Queller, D.C.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1996) Ecology & Evolutionary Biology, Rice University, 6100 Main, Houston, TX 77005, USA
FEATURES
source Location/Qualifiers
1..255
/organism="Parachartergus colobopteranus"
/clone="Paco3301CAT"
satellite 1..255
/note="microsatellite"
primer_bind complement(137..156)
repeat_region 164..208
primer_bind 236..255
BASE COUNT 59 a 57 c 90 g 49 t
ORIGIN
Query Match 2.0%; Score 31; DB 204; Length 255;
Best Local Similarity 100.0%; Pred. No. 3,44e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 179 tgtatgatgatgatgatgatgatgatg 209
|||||
Cp 37 TGTGATGATGATGATGATGATGATG 7
RESULT 7
LOCUS G08117 256 bp DNA STS 08-AUG-1995
DEFINITION human STS CHLC.ATC3E01.P7574 clone ATC3E01.
ACCESSION G08117
NID 9938667
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo Sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 256)
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: ATC3E01, CHLC.ATC3E01.#T7573
CONTACT: Dr. Jeffrey C. Murray
DOI The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@iowa.edu
Primer A: GCTGGCATGATAATTCCT
Primer B: AAATGGCCACTCCCTAAAC
STS size: 147
PCR Profile: denature: 30 seconds at 94 degrees C

annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 uL
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.
Location/Qualifiers
1..256
/organism="Homo Sapiens"
source
STS 7..153
primer_bind 7..26
primer_bind complement(134..153)
BASE COUNT 58 a 37 c 62 g 80 t 19 others
ORIGIN
Query Match 2.0%; Score 31; DB 196; Length 256;
Best Local Similarity 100.0%; Pred. No. 3,44e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 78 tgatgatgatgatgatgatgatgatg 108
|||||
Cp 35 TGATGATGATGATGATGATGATGATG 5
RESULT 8
LOCUS HSB346YB5 298 bp DNA STS 24-MAR-1996
DEFINITION H.sapiens (DIS2781) DNA segment containing (CA) repeat; clone AFMB346YB5; single read.
ACCESSION 253778
NID 91235224
KEYWORDS CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism; STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 298)
AUTHORS Weissenbach, J.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
E-mail: Jean.Weissenbach@genethon.fr
REFERENCE 2 (bases 1 to 298)
AUTHORS Dib, C., Faure, S., Fizames, C., Samson, D., Drouot, N., Vignal, A., Millasseau, P., Marc, S., Hazan, J., Seboun, E., Lathrop, M., Gyapay, G., Morissette, J. and Weissenbach, J.
TITLE A comprehensive genetic map of the human genome based on 5,264 microsatellites
JOURNAL Nature 380 (6570), 152-154 (1996)
MEDLINE 96176476
COMMENT full automatic.
FEATURES
source Location/Qualifiers
1..298
/organism="Homo sapiens"
/note="Cloning vector is M13mp18"
/cell_line="CEPH 134702"
/clone_id="genomic DNA"
/chromosome="1"

BASE COUNT 90 a 107 c 33 g 66 t 2 others
ORIGIN
Query Match 2.0%; Score 31; DB 203; Length 298;
Best Local Similarity 97.0%; Pred. No. 3,44e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db	212	catcatcatcatcatcatcatcatcatcatcagc	244
0y	7	CATCATCATCATCATCATCATCATCATCATCAGC	39
RESULT	9		
LOCUS	G08591	314 bp	DNA
DEFINITION	human STS CHLC.ATC6.P9593 clone ATC6.		STS
ACCESSION	G08591		
NID	9359141		
KEYWORDS	STS sequence; primer; sequence tagged site.		
SOURCE	human vector-pJc1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.		
ORGANISM	Homo Sapiens		
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates		
REFERENCE	1 (bases 1 to 314)		
AUTHORS	Murray,J., Sheffield,V., Weber,J.L., Duyk,G. and Buettow,K.H.		
TITLE	Cooperative Human Linkage Center		
JOURNAL	Unpublished (1995)		
COMMENT	Synonyms: ATC6, CHLC.ATC6.#P9592		
	Contact: Dr. Jeffrey C. Murray		
	UofI		
	The University of Iowa		
	Department of Pediatrics, Iowa City, IA 52242, USA		
	Tel: (319) 356-3508		
	Fax: (319) 356-3347		
	Email: jeff-murray@uiowa.edu		
	Primer A: AGTACTGTGTAAGAGTGCCTGGC		
	Primer B: GAAATTTTCTGGACCTGGCA		
	STS size: 105		
	PCR Profile:		
	denature: 30 seconds at 94 degrees C		
	annealing: 75 seconds at 55 degrees C		
	extension: 15 seconds at 72 degrees C		
	PCR cycles: 27		
	extension: 6 minutes at 72 degrees C		
	Protocol:		
	Template: 30ng genomic DNA		
	Primer: each 1.5 pmole		
	dNTPs: each 200 uM		
	Taq Polymerase: 0.3 units		
	Total Vol: 10 ul		
	Buffer:		
	MgCl2: 1.5mM		
	KCl: 50mM		
	Tris: 10mM		
	pH: 8.3		
FEATURES			
source	Location/Qualifiers		
STS	1..314		
primer_bind	/Organism="Homo Sapiens"		
primer_bind	54..158		
primer_bind	54..75		
BASE COUNT	complement(139..158)		
ORIGIN	72 a 87 c 46 g 102 t 7 others		
Query Match	2.0%; Score 32; DB 197; Length 314;		
Best Local Similarity 100.0%; Pred. No. 1.07e-16;			
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	73	ggccatcatcatcatcatcatcatcatcatcatca	104
0y	4	GCCATCATCATCATCATCATCATCATCATCA	35

LOCUS	10	G09253	377 bp	DNA	STS	14-AUG-1995
DEFINITION		human STS CHLC.ATC2F09.P7509 clone ATC2F09.				
ACCESSION		G09253				
NID		g941102				
KEYWORDS		STS sequence; primer; sequence tagged site.				
SOURCE		human vector-pUCPI host-E.coli dut-ungr (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.				
AUTHORS		1 (bases 1 to 377)				
TITLE		Murray,J., Sheffield,V., Weber,J.L., Dnyk,G. and Buetow,K.H.				
JOURNAL		Cooperative Human Linage Center				
COMMENT		Unpublished (1995) Synonyms: ATC2F09, CHLC.ATC2F09.T7508 Contact: Dr. Jeffrey C. Murray UofI The University of Iowa Department of Pediatrics, Iowa City, IA 52242, USA Tel.: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu Primer A: ACCAAGCACTGAGTGCAGCG Primer B: CTCGACTCCAGAGCTCGTCGT STS size: 164 PCR Profile: denature: 30 seconds at 94 degrees C annealing: 75 seconds at 55 degrees C extension: 15 seconds at 72 degrees C PCR cycles: 27 extension: 6 minutes at 72 degrees C Template: 30ng genomic DNA Primer: each 1.5 pmole dNTPs: each 200 uM Tag Polymerase: 0.3 units Total Vol: 10 ul Buffer: MgCl2: 1.5mM KCl: 50mM Tris: 10mM pH: 8.3. Location/Qualifiers 1..377 /organism="Homo sapiens" STS primer_bind 44..207 44..63 BASE COUNT 74 a 90 c 90 g 105 t 18 others ORIGIN Query Match 2.0%; Score 31; DB 197; Length 377; Best Local Similarity 80.0%; Pred.No. 3,44e-15; Matches 48; Conservative 0; Mismatches 11; Indels 1; Gaps 11. Db 91 ccacatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcgttgtcgctca 150 Oy 6 ccattcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcatcat 64 RESULT 11 LOCUS ATTS1025 514 bp RNA EST 13-AUG-1993 DEFINITION A. thaliana transcribed sequence; clone GBG87. ACCESSION Z25512 NID g396648 KEYWORDS expressed sequence tag; partial cDNA sequence.				

SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Caperales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 514)
AUTHORS Quigley and Maché, R.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1993) CNRS, GDR-1003 ACS, INRA, Laboratoire de
Biologie Moléculaire, BP 27, 31326 Castanet-Tolosan cedex, France.
E-mail: gdr-sy@toulouse.inra.fr. On behalf of: CNRS URA 1178,
Laboratoire de Biologie Moléculaire végétale, B.P. 53X, 38041
Grenoble Cedex, France. E-mail: FOUIGHEY@grenet.fr
2 (bases 1 to 514)
CNRS.
REFERENCE The Arabidopsis thaliana transcribed genome: the GDR cDNA program
AUTHORS Unpublished
TITLE Cloning vector: Lambda ZAP11.;
JOURNAL full automatic.
COMMENT Location/Qualifiers
FEATURES
source 1..514
/organism="Arabidopsis thaliana"
/clone="GB8687"
/tissue_type="Flower buds of A.thaliana ecotype columbia
C24"
/clone_lib="Grenoble-B"
BASE COUNT 153 a 101 c 114 g 146 t
ORIGIN
Query Match 2.0%; Score 31; DB 19; Length 514;
Best Local Similarity 97.0%; Pred. No. 3,44e-15;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 431 atcatcatcatcatcatcatcatcatcatca 463
|||||
OY 8 ATCATCATCATCATCATCATCATCATCATCA 40
RESULT 12
LOCUS HUMUT7996 521 bp DNA STS 28-DEC-1994
DEFINITION Human STS UT7996.
ACCESSION L30172
NID 9605349
KEYWORDS PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; trinucleotide repeat.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
White, R.
TITLE Genetic and physical mapping of simple sequence repeat containing
sequence tagged sites from the human genome
JOURNAL Unpublished (1994)
COMMENT Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: ATTCCCGGCTTGGCCGC
Primer B: GAAGAATGTCCTCATCATG
End to Label: Primer B
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation: 64 C 10 sec. Annealing 72 C 20 sec. 30
C 10 sec. 58 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 1.
Location/Qualifiers
FEATURES
source 1..521
/organism="Homo sapiens"
/standard_name="STS UT7996"
primer_bind 151..169
primer_bind /evidence=experimental
complement(308..328)
/evidence=experimental
BASE COUNT 103 a 163 c 103 g 143 t 9 others
ORIGIN
Query Match 2.0%; Score 32; DB 204; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.07e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 207 ggcacatcatcatcatcatcatcatcatca 238
|||||
OY 4 GGCCATCATCATCATCATCATCATCATCA 35

SOURCE 1..521
/organism="Homo sapiens"
STS 151..328
/standard_name="STS UT7996"
primer_bind 151..169
primer_bind /evidence=experimental
complement(308..328)
/evidence=experimental
BASE COUNT 103 a 163 c 103 g 143 t 9 others
ORIGIN
Query Match 2.0%; Score 32; DB 204; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.07e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 207 ggcacatcatcatcatcatcatcatcatca 238
|||||
OY 4 GGCCATCATCATCATCATCATCATCATCA 35

RESULT 14
LOCUS 609471 588 bp DNA STS 14-AUG-1995
DEFINITION human STS CHLC.ATC5A05.P10592 clone ATC5A05.
ACCESSION G09471
NID 6941320
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pUCP1 host-E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Homiidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buettow,K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1985)
COMMENT Synonyms: ATC5A05, CHLC.ATC5A05.T10591
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
Primer A: AATGTCATCACCTTCTCTCC
Primer B: TGTGTGAGCTGAGATTTGTG
STS size: 199
PCR Profile:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Tag Polymerase: 0.3 units
Total Vol: 10 ul
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.
Location/Qualifiers
source 1..588
/Organism="Homo sapiens"
STS 23..221
primer_bind complement(202..221)
BASE COUNT 108 a 151 c 95 g 184 t 50 others
ORIGIN
Query Match 2.0%: Score 31; DB 197; Length 588;
Best Local Similarity 100.0%; Pred. NO. 3,44e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 136 atcatcatcatcatcatcatcatcacg 166
|||||
OY 8 ATCATCATCATCATCATCATCATCAG 38

RESULT 15
LOCUS 609999 277 bp DNA STS 14-AUG-1995
DEFINITION human STS CHLC.GCT16B04.P18276 clone GCT16B04.
ACCESSION G09999
NID 9941848
KEYWORDS STS sequence; primer; sequence tagged site.

SOURCE human vector-pUCP1 host-E.coli dut+ung+ (DH10B) Marker Selected
genomic DNA prepared from XY individual of French nationality.
ORGANISM Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Carnivora; Homiidae; Homo.
REFERENCE 1 (bases 1 to 277)
AUTHORS Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buettow,K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: GCT16B04, CHLC.GCT16B04.T18143
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu
Primer A: CCCCTCTGTTTCCAACTT
Primer B: TGTGATACAAATTAGCAAGC
STS size: 142
PCR Profile:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Tag Polymerase: 0.3 units
Total Vol: 10 ul
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3.
Location/Qualifiers
source 1..277
/Organism="Homo sapiens"
STS 6..147
primer_bind complement(125..147)
BASE COUNT 70 a 50 c 63 g 94 t
ORIGIN
Query Match 1.9%: Score 30; DB 197; Length 277;
Best Local Similarity 94.9%; Pred. NO. 1.04e-13;
Matches 37; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Db 55 gctcgtcgtcgtgatgatgatgatgatgatgat 93
|||||
Cp 45 GCCGCTGCTG-TGATGATGATGATGATGATGAT 8

Search completed: Fri Apr 25 19:13:56 1997
Job time : 1016 secs.

Release 2:ID John F. Collins, Biocomputing Research Unit.
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Title: >US-08-699-716A-2
Description: (1-521) from US08699716A.pep
Perfect Score: 3546
Sequence: 1 MGNINNNNNNNHSSGIDDD.....RTQKIVDSWQRLDLDTSGK 521

```

Searched: 88003 seqs, 10295656 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq25

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18

Statistics: Mean 35.391; Variance 190.955; scale 0.185

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2242	63.2	329	15	R75961	Partial Lcrv (V anti	3.48e-16
2	2233	63.0	329	15	R75962	Partial Lcrv (V anti	1.80e-16
3	1100	3.0	170	14	R76528	Yersinia pestis cagl	5.61e-74
4	968	27.3	151	14	R76526	Yersinia pestis cagl	1.17e-63
5	966	27.2	151	14	R76527	Yersinia pestis cagl	1.67e-63
6	150	4.2	462	17	R95009	Type A neurotoxin C f	3.06e-02
7	110	3.1	835	17	R96206	Invasin protein.	9.84e-00
8	106	3.0	174	17	R85503	Borrelia burgdorferi	1.70e+01
9	108	3.0	455	10	R57771	Mouse nucleobindin.	1.70e+01
10	105	3.0	493	3	R13992	F. falcatiparum sporozo	1.95e+01
11	106	3.0	708	2	R08402	Amil15 encoded by Ida	1.70e+01
12	105	3.0	2482	14	R72826	Human mt10s1n.	1.70e+01
13	105	3.0	3248	18	R93795	Kinectochore protein C	1.95e+01
14	103	2.9	257	7	R36675	30 kb Borrelia burgdo	2.55e+01
15	103	2.9	663	3	R13139	B.burgdorferi strain	2.55e+01
16	102	2.9	1529	18	R97985	CORF pocassus1m channe	2.92e+01
17	99	2.8	672	5	R31216	Penicillin binding pr	4.36e+01
18	100	2.8	793	4	R20743	Murine receptor-type	3.82e+01
19	100	2.8	793	18	M02282	Murine receptor type	3.82e+01
20	100	2.8	802	18	M02283	Human receptor type P	3.82e+01
21	100	2.8	802	4	R20744	Human receptor type P	3.82e+01

ALIGNMENTS

RESULT 1
ID R79961 standard; Protein: 329 AA.
AC R79961;
DT 18-APR-1996 (first entry)
DE Partial Lcrv (V antigen) of Y. pestis.
KW Lcrv; V antigen; virulence; plague; vaccine; epitope.
OS Yersinia pestis.
PN W09524475-A1.
PD 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MIMA) UK SEC FOR DEFENCE.
PI Leary SEC, Tilchall RW, Williamson ED, Leary SE;
DR WPI: 95-328268/42.
DR N-PSDB: T04222.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
PT oral or parenteral vaccines for protection against plague
PS Claim 6: Page 11-13; 25pp: English.
CC R79961-62 are encoded by T04222-23 (resp.), DNA sequences (lcrv) encoding
CC all or a protective epitopic part of the mature V protein of Yersinia
CC pests. The protein was expressed as a fusion protein with maltose
CC binding protein or glutathione-S-transferase in 3 different plasmid
CC vectors. Y. pestis is the highly virulent causative organism of plague
CC in a wide range of animals, including man. The V antigen (Lcrv) is an
CC unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb Lcr plasmid.
CC The V antigen is postulated to act as a virulence antigen, and
CC transformed microorganisms contg. recombinant DNA encoding a V antigen
CC protein/peptide are useful in vaccines to protect against plague.
SQ Sequence 329 AA;

	Query Match	63.2%	Score 2242;	DB 15;	Length 329;
	Best Local Similarity	99.4%	Pred. No. 3,486-164;		
	Matches 326;	Conservative 1;	Mismatches 0;	Indels 1;	Gaps 1.;
Db	3 ef-irayeqnqphiedlekryveqetlgbssvleelvgivdknidtsikypdkse	61			
Qy	194 EFMIRAEQNGQHIEDLEKRYVBQLGHSSTVLEELVLYKKNIDISIKYPRKSEV	253			
Db	62 faanvttddlellkkilayfipegaillkgghydnqilngikryvkefiesspntqwe	121			
Qy	254 FANRVITDDIELLKKILAYFLPEDTILKGGHYDNQNGIKRYVKEFIESSPNTQWELRAF	313			
Db	122 mavmhfsitadriiddllklyvdsamnhgdarskllreelaeltaelklysviqaein	181			
Qy	314 MAVMHFSITADRIIDDILKLYVDSAMNHGARSKLLREELAEELKLYSVIQAEIKHLL	373			

Db 182 sssgtinhdksinlmdknlgytdeelfkaseaykilekmpgttqvgdsekkivskd 241
|||||
QY 374 SSSGTINHDKSNLMDKNLGYTDEELFKASEAYKILEKMPGTTIQVGSEKKIVSIND 433
Db 242 ffgsenkrtgalgnknsysynkdneshfatccsdksrplndlvsgkttqtsdltstrf 301
|||||
QY 434 FLGSEKRRFGALGNLKNLSYKNNNELSHFATTCSDKSRPLNDLVSGKTTQTSIDTISRf 493
Db 302 nsaiealnrfikkydsvmgrllldtsgk 329
|||||
QY 494 NSAIETALNRFIOKRYDSVMORLDDTSGK 521

RESULT 2
ID R79962: standard; Protein: 329 AA.

AC R79962: 18-APR-1996 (first entry)
DE Partial lcrv (V antigen) of Y. pestis.
KW lcrv; V antigen; virulence; plague; vaccine; epitope.
OS Yersinia pestis.
PN WO9524475-A1.
PD 14-SEP-1995.
PF 06-MAR-1995; G00481.
PR 08-MAR-1994; GB-004577.
PA (MINA) UK SEC FOR DEFENCE.
PI Leary SEC, Titball RW, Williamson ED, Leary SE;
DR WPI: 95-3328268/42.
DR N-PSDB: T04223.
PT Recombinant DNA expressing Yersinia pestis V antigen - useful in
oral or parenteral vaccines for protection against plague
PS Claim 6; Page 15-16; 25pp; English.
CC R79961-62 are encoded by T04223-23 (resp.), DNA sequences (lcrv) encoding
all or a protective epitopic part of the mature V protein of Yersinia
pestis. The protein was expressed as a fusion protein with maltose
binding protein or glutathione-S-transferase in 3 different plasmid
vectors. Y. pestis is the highly virulent causative organism of plague
in a wide range of animals, including man. The V antigen (lcrv) is an
unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb lcr plasmid.
CC The V antigen is postulated to act as a virulence antigen, and
transformed microorganisms contg. recombinant DNA encoding a V antigen
protein/peptide are useful in vaccines to protect against plague.
SQ Sequence 329 AA;

Query Match 63.0%; Score 2233; DB 15; Length 329;
Best Local Similarity 99.4%; Pred. No. 1,80e-163;
Matches 323; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 5 lrayeqnpqhlledlekvrveqltghssvleelvglvkdknidisikydprkxsevfaf 64
|||||
QY 197 IRAYEQNPQHLEDELEKVRVEQLTGHSSVLEELVGLVKDNIDISIKYDPRKXSEVFAN 256
Db 65 rvtlddellekhllyflpedallkghydnqngikrvkeflesspntqwelirafmay 124
|||||
QY 257 RVTLDDELEKHLFLPEDELLKGYHNDQNGIKRVEFLESSPNTQWELIRAFMAY 316
Db 125 mhfsltadtidddllkvtidsmnhghdarskireelaqtaelklysvigaelnkhlss 184
|||||
QY 317 MHFSLTADRIDDDILKVIYDSNMHHHDARSKLREELAEELTAEIKTISVQAEINKHLSSS 376
Db 185 grlnhdksinlmdknlgytdeelfkaseaykilekmpgttqvgdsekkivskd 244
|||||
QY 377 GRINHDKSNLMDKNLGYTDEELFKASEAYKILEKMPGTTIQVGSEKKIVSIND 436
Db 245 senkrtgalgnknsysynkdneshfatccsdksrplndlvsgkttqtsdltstrf 304
|||||
QY 437 SENKRTGALGNLKNLSYKNNNELSHFATTCSDKSRPLNDLVSGKTTQTSIDTISRf 496
Db 305 lealnrfikkydsvmgrllldtsgk 329
|||||
QY 497 IEALNRFIOKRYDSVMORLDDTSGK 521

RESULT 3
ID R76528: standard; Protein: 170 AA.

AC R76528: 17-DEC-1995 (first entry)
DE Yersinia pestis cafi (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN WO9518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 95-246396/32.
DR N-PSDB: Q92819.
PT DNA constructs capable of transforming microorganisms - which can be
used as live or attenuated vaccines which induce an immune response,
against Yersinia pestis, at mucosal surfaces.
PS Disclosure: Page 20; 27pp; English.
CC The sequence represents the Y. pestis cafi (F1) antigen expressed
from plasmid pPROFib. The DNA construct can be used to transform
human or animal gut colonizing microorganisms, specifically
attenuated Salmonella typhimurium or Salmonella typhi. The
transformed microorganisms can be used as live/attenuated vaccines
CC which induce immune responses at mucosal surfaces. The vaccines
provide protection against infection with Y. pestis, and are
parenterally and orally active vaccines offering protection
against bubonic and pneumonic plague.
SQ Sequence 170 AA;

Query Match 31.0%; Score 1100; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 5.61e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkksivialafglatanaadlastatatlvepariltlykegapltmdnqndt 60
|||||
QY 24 MKKISSVIALFGIATVANAADLASTATATVEPARILTLYKEGAPITMDNGNIDT 83
Db 61 ellvgtlclgykctttsvntftdaagdpmylittsgdgmnhqftkvyigkdsrddis 120
|||||
QY 84 ELLVGTLLTGKTKTGTTSVNEFTDAAGDPMYLFTPSDGNHGHPTTRVIGKDSRDPDIS 143
Db 121 pkvgenlvgddvlatysqdfvrsiskgkllaqkytdavtyvsnq 170
|||||
QY 144 PKVGENLVGDDVVLATGSQDFVRISISGSKGLAQRITDAVTVTSNQ 193

RESULT 4
ID R76526: standard; Protein: 151 AA.

AC R76526: 17-DEC-1995 (first entry)
DE Yersinia pestis cafi (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KW bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN WO9518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Titball RW, Williamson ED;
DR WPI: 95-246396/32.
DR N-PSDB: Q92817.
PT DNA constructs capable of transforming microorganisms - which can be
used as live or attenuated vaccines which induce an immune response,
against Yersinia pestis, at mucosal surfaces.
PS Disclosure: Page 16; 27pp; English.
CC The sequence represents the Y. pestis cafi (F1) antigen expressed
from plasmid pFGL2a. The DNA construct can be used to transform
human or animal gut colonizing microorganisms, specifically
attenuated Salmonella typhimurium or Salmonella typhi. The
transformed microorganisms can be used as live/attenuated vaccines

CC Which induce immune responses at mucosal surfaces. The vaccines
CC provide protection against infection with Y. pestis, and are
CC parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 151 AA;

Query Match 27.3%; Score 968; DB 14; Length 151;
Best Local Similarity 96.0%; Pred. No. 1.17e-63;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 ssadltatattatlveparitltvkegapitlmdngnidellvgtlltggvktgttst 60
QY NADLTATATATATVETPARITLTKEGAPITMDNGNIDELLVGTLLGKGTGTST 102
Db 61 svnfdaagdpmylftfsqgdnbqfttkvlgksrdldispkngenlvagddvlatgs 120
QY VNFETDAAGDPMYLFTFSQGNBHQFTTKVIGKSRDLDISPKNENLVAGDDVLTATGS 162
Db 121 qdftvrsigskgkllaagkytdavtvtsnq 151
QY 163 QDEFVRSIGSKGKLLAAGKYTDVTVTSNQ 193

RESULT 5

ID R76527 standard; Protein; 151 AA.
AC R76527;
DT 17-DEC-1995 (first entry)
DE Yersinia pestis cafI (F1) antigen.
KW Vaccine; antigen; Salmonella typhimurium; Salmonella typhi;
KM bubonic plague; pneumonic plague.
OS Yersinia pestis.
PN W09518231-A1.
PD 06-JUL-1995.
PF 23-DEC-1994; G02818.
PR 24-DEC-1993; GB-026425.
PA (MINA) UK SEC FOR DEFENCE.
PI Howells A, Leary SEC, Oyston PCF, Tiltball RW, Williamson ED;
DR WPI; 95-246396/32.
DR N-PSDB; Q92818.
PT DNA constructs capable of transforming microorganisms - which can be
PT used as live or attenuated vaccines which induce an immune response,
PT against Yersinia pestis, at mucosal surfaces.
PS Disclosure; Page 18; 27pp; English.
CC The sequence represents the Y. pestis cafI (F1) antigen expressed
CC from plasmid pF132a. The DNA construct can be used to transform
CC human or animal gut colonizing microorganisms, specifically
CC attenuated Salmonella typhimurium or Salmonella typhi. The
CC transformed microorganisms can be used as live/attenuated vaccines
CC which induce immune responses at mucosal surfaces. The vaccines
CC provide protection against infection with Y. pestis, and are
CC parenterally and orally active vaccines offering protection
CC against bubonic and pneumonic plague.
SQ Sequence 151 AA;

Query Match 27.2%; Score 966; DB 14; Length 151;
Best Local Similarity 96.7%; Pred. No. 1.67e-63;
Matches 148; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 padltatatatlveparitltvkegapitlmdngnidellvgtlltggvktgttst 61
QY AADLTATATATVETPARITLTKEGAPITMDNGNIDELLVGTLLGKGTGTST 103
Db 62 vnfdaagdpmylftfsqgdnbqfttkvlgksrdldispkngenlvagddvlatgs 121
QY VNFETDAAGDPMYLFTFSQGNBHQFTTKVIGKSRDLDISPKNENLVAGDDVLTATGS 163
Db 122 qdftvrsigskgkllaagkytdavtvtsnq 151
QY 164 DFEVRSIGSKGKLLAAGKYTDVTVTSNQ 193

RESULT 6
ID R95009 standard; Protein; 462 AA.

AC R95009;
DT 07-JUL-1996 (first entry)
DE Type A neurotoxin C fragment-polystyridine tag fusion pHisBot.
KW Toxin; neurotoxin; fusion protein; antitoxin; vaccine; immunogen;
KM Clostridium botulinum; polystyridine; vector; pPTHisa; pHisBot.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Polystyridine-tag
FT Protein 22..462
FT /label= C-fragment
PN W09612802-A1.

PD 02-MAY-1996.
PF 23-OCT-1995; 013737.
PR 24-OCT-1994; US-329154.
PR 16-MAR-1995; US-405496.
PR 14-APR-1995; US-422711.
PR 07-JUN-1995; US-480604.
PA (OPH-) OPHIDIAN PHARM INC.
PI Firca JR, Kink JA, Padhye NV, Stafford DC, Thalley BS;
PI Williams JA;
DR WPI; 96-230603/23.
DR N-PSDB; T29246.
PT Fusion proteins comprising non-toxin protein and part of toxin -
PT useful to form anti-toxins against Clostridium botulinum type A, and
PT C. difficile type toxins, and to treat C. difficile intoxication,
PT paric. diarrhoea
PS Claim 7; Page 340-342; 434pp; English.
CC PhisBot fusion protein (R95009), the product of a nucleotide
CC sequence (729246) in vector pPTHisa, comprises a polystyridine
CC affinity tag and fragment C (see also R95008) of the Clostridium
CC botulinum type A neurotoxin. The PhisBot protein was expressed
CC in Escherichia coli as a soluble protein and was purified by
CC metal chelate affinity chromatography to obtain a product free
CC of endotoxin contamination that may be useful as an immunogen
CC in vaccine compns.
SQ Sequence 462 AA;

Query Match 4.2%; Score 150; DB 17; Length 462;
Best Local Similarity 59.4%; Pred. No. 3.06e-02;
Matches 19; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

Db 1 mghhhhhhhhsgnleg--rhmasmarlls 30
QY 1 MGHNNHHHHSSGHDDDKMKKRISYIA 32

RESULT 7

ID R96206 standard; Protein; 835 AA.
AC R96206;
DT 24-AUG-1996 (first entry)
DE Invasin protein.
KW Invasin; drug delivery; gastrointestinal membrane; transcytosis;
KW bioavailability; fusion protein; enterocyte; Peyers patch M-cell.
OS Yersinia enterocolitica strain 8081c.
FH Key Location/Qualifiers
FT Region 645..835
FT /note= "C-terminal receptor binding region"
PN W09613250-A1.
PD 09-MAY-1996.
PF 20-OCT-1995; 013749.
PR 27-OCT-1994; US-331393.
PA (AMGE-) AMGEN INC.
PI Habbelfield AD, Jensen-Piippo K;
DR WPI; 96-251447/25.
DR N-PSDB; T27535.
PT Therapeutic delivery system utilising bacterial invasin protein - is
PT not readily degraded in the gut, enhances systemic bio-availability
PT of therapeutic agents
PS Example 1; Fig 1; 110pp; English.
CC The sequence represents a bacterial invasin protein, which may be
CC complexed with a therapeutic agent to transport the agent across
CC the gastrointestinal membrane barrier by transcytosis to increase

CC bioavailability 5- to 100-fold. The agent and bacterial protein
CC may be linked via a degradable peptide sequence as a fusion
CC protein. The receptor binding region of the invasion protein
CC involves the 192 amino acids at the C-terminal end of the protein.
CC This region retains the binding affinity of the protein, and may be
CC used alone or as part of a fusion protein for drug delivery. The
CC binding region may be fused with maltose binding protein (R96208)
CC to form a fusion protein (R96209) which may be purified easily by
CC amylose affinity chromatography. The delivery system allows
CC improved transport across enterocytes and Peyer's patch M-cells.
CC The system is not prone to degradation in the gut or early release
CC of biologically active material, and eliminates the need for
CC parental administration.
SQ Sequence 835 AA;

Query Match 3.18; Score 110; DB 17; Length 835;
Best Local Similarity 25.88; Pred. No. 9.84e+00;
Matches 33; Conservative 43; Mismatches 42; Indels 10; Gaps 8;

Db 509 gysialtsftvgsvvtldigqgqtvrrfvlppdtinsfnspdiavdgsmgi 568
QY 29 SYVALNLFETATATANA-DLTRS-TTATATL-VEPARITLYKBCAPITIMNGNIDIE 84
Db 569 ltfvprknefysgldt--lefigs-gvpvtispvtenadn--tyasvgnsgqvdi 623
QY 85 L-LVGTFLTIGYKKTGTSTSVNFTDAAGDPMVLTFTSQDGNHQTXTVIGKDSRFDIS 143
Db 624 pvyggesl 631
QY 144 PKVNGENTL 151

RESULT 8
ID R88503 standard; Protein: 174 AA.
AC R88503;
DT 31-JUL-1996 (first entry)
DE Borrelia burgdorferi exported plasmid protein A (Eppa).
KW Eppa; Lyme disease; antigenic; immune response; detection; virulent;
infection.
OS Borrelia burgdorferi.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label- sig_peptide
FT Protein 21..174
FT /label- mat_protein
FN W09535114.1.
PD 28-DEC-1995.
PF 16-JUN-1995; U07748.
PR 17-JUN-1994; US-261825.
PA (REGC) UNIV CALIFORNIA.
PI Blanco DR, Champion CI, Haake DA, Lovett MA, Miller JW;
DR WPI: 96-058208/06.
DR N-PSDB; T10931.
PT Borrelia burgdorferi exported plasmid protein A - used to develop
PT prods. to induce an immune response to B.burgdorferi and as
PT diagnostic markers for Lyme disease
PS Claim 3: Page 46, Fig 2; 67pp; English
CC R88503 represents the Borrelia burgdorferi, exported plasmid
CC protein A (Eppa). Eppa is a virulent protein of about 17 kD.
CC Eppa and its active fragments can be used to induce an animal.
CC response to pathogenic Borrelia burgdorferi (BB) in an animal.
CC The sequence may be used to produce recombinant Eppa expressed
CC in E. coli. Eppa is exported beyond the inner membrane and is
CC present during the infectious, in vivo stages of virulent BB
CC growth. Polynucleotides encoding Eppa and anti-Eppa antibodies
CC can be used for the detection of pathogenic BB in a sample.
SQ Sequence 174 AA;

Query Match 3.08; Score 106; DB 17; Length 174;
Best Local Similarity 34.58; Pred. No. 1.70e+01;
Matches 20; Conservative 12; Mismatches 24; Indels 2; Gaps 2;
Db 115 lkgypnsitfdylqlsdsk-idyaekyge-karenfeesykkxklavkqilxqlad 170

QY 219 LGHSSVLEELHVLQVJWKKNIDISIKYDPKDSVFANRVITDIELKKILAYPLPE 276

RESULT 9
ID R57771 standard; Protein: 455 AA.
AC R57771;
DT 21-SEP-1994 (first entry)
DE Mouse nucleobindin.
KW Nuc protein; nucleobindin; antibody; autoimmune disease;
KW augmenting factor; DNA binding; p53.
OS Mus musculus.
PN J06025292-A.
PD 01-FEB-1994.
PF 30-OCT-1991; 349306.
PR 31-OCT-1990; JP-294055.
PR 26-NOV-1990; JP-324888.
PA (GAKU/) GAKUEN F.
PA (MTRK) MITSUI TOATSU CHEM INC.
PA (YOSH-) YOSHIIYUKI KANAI GH.
DR WPI: 94-077375/10.
DR N-PSDB; Q67223.
PT Anti-DNA antibody prodn. augmenting factor - and antibodies to
PT it, useful for diagnosis and treatment of autoimmune disease
PS Disclosure: Fig 7; 29pp; Japanese.
CC Nuc protein binds DNA and augments anti-DNA antibody prodn. The
CC protein is from human or mouse tissue or cells, esp. lymphocytes.
CC Anti-nuc protein antibodies may be used to treat diseases involving
CC prodn. of large amts. of DNA binding protein, e.g. autoimmune
CC disease.
SQ Sequence 455 AA;

Query Match 3.08; Score 108; DB 10; Length 455;
Best Local Similarity 19.88; Pred. No. 1.30e+01;
Matches 36; Conservative 57; Mismatches 82; Indels 7; Gaps 7;

Db 223 sqagklveveelgdldnfnfkftffihndinsdgvldgelealfteklekyqpknee 282
QY 344 ARSKRLRELAELTA-ELKIVSYQAEINKHLSSSGTINH-D-KSINLMD-KLVGYTDEE 400
Db 283 ddmremeeerlmrehymknvtdngdrjvleeflastrkefgdtgqkwtempayt 342
QY 401 IFKASAEYKILBKMPQTTQVDGSEKKIVSIRKDFGSEKKRT-GALGN-LKN-SYSYND 457
Db 343 eeeLkrfeeeLaareelna-ragrlsgetealysqdtleaqkrelqgmqrkqlqeq 401
QY 458 NNELSHFATTCSDKSRPLNDLVSOQTQDLSITSRNSAIEALNRFIOKYDSVMQRLDD 517
Db 402 sa 403
QY 518 TS 519

RESULT 10
ID R13992 standard; Protein: 493 AA.
AC R13992;
DT 05-DEC-1991 (first entry)
DE P. falciparum sporozoite antigen fusion polypeptide.
KW Vaccine; NXY gene; malaria; antibodies; purification; affinity.
OS Plasmodium falciparum.
FH Key Location/Qualifiers
FT Region 1..21
FT /label- A
FT /note- "affinity peptide including 6 His residues"
FT Region 22..483
FT /label- B
FT /note- "amino acids 1-462 of the peptide in R13991"
FT Region 484..493
FT /label- C
FT /note- "vector-encoded_peptide"
FN EP-447956-A.
PD 25-SEP-1991.
PF 14-MAR-1991; 103920.

1
2
3
4

5

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2245	63.3	326	9	B33601	lcrv protein - Yersinia	9.45e-28
2	2192	61.8	326	9	B37314	regulatory protein L	2.08e-27
3	1100	31.0	170	9	S133008	capsular antigen F1	1.88e-12
4	168	4.7	168	13	I58315	Wfl - human	4.08e-05
5	127	3.6	168	9	S57904	CS3 pilin precursor	3.73e-01
6	127	3.6	116	11	S57382	hypothetical protein	3.73e-01
7	123	3.5	168	9	A34952	CS3 fimbrin protein	8.48e-01
8	123	3.5	489	7	S47608	actin homolog YJ1081	8.48e-01
9	124	3.5	857	12	S13821	median body protein	6.92e-01
10	123	3.5	2076	12	S15899	fatty-acyl-CoA synth	8.48e-01
11	120	3.4	220	11	S48450	hypothetical protein	1.56e+00
12	120	3.4	333	3	K1BR56	ribokinase (EC 2.7.1	1.56e+00
13	121	3.4	411	14	I58156	Bmr-3.2 - mouse	1.27e+00
14	119	3.4	2529	12	A56923	transcription factor	1.90e+00
15	119	3.4	2578	12	A56922	transcription factor	1.90e+00
16	118	3.3	264	13	S34121	transcription factor	2.32e+00
17	118	3.3	410	13	I38502	DNA-Bmr-3b protein	2.32e+00
18	116	3.3	650	5	I34181	gene-directed RNA pol	3.44e+00
19	117	3.3	1302	16	JC6009	surface-located memb	2.83e+00
20	115	3.2	812	11	A46417	NIP1 protein - yeast	4.19e+00
21	111	3.1	311	12	S25163	gamma-glardin - Glar	9.08e+00

45	107	3.0	1300	9	S07575
44	107	3.0	911	11	S51441
43	106	3.0	855	14	I59350
42	106	3.0	756	9	A32976
41	108	3.0	729	3	A34796
40	105	3.0	714	10	C64339
39	108	3.0	577	5	B44307
38	108	3.0	455	14	UC1224
37	107	3.0	385	11	S6587
36	106	3.0	375	11	A65390
35	106	3.0	325	11	A46887
34	106	3.0	351	16	S62602
33	106	3.0	288	4	JQ1877
32	106	3.0	174	8	I40244
31	110	3.1	1175	10	F64489
30	109	3.1	1109	8	A56143
29	111	3.1	1004	10	D25039
28	111	3.1	982	10	I64232
27	111	3.1	973	11	S54534
26	110	3.1	835	9	S54412
25	110	3.1	835	9	S11446
24	109	3.1	711	9	B61469
23	110	3.1	588	9	H64046
22	110	3.1	384	9	S18535
21	110	3.1	384	9	S18535
20	110	3.1	384	9	S18535
19	110	3.1	384	9	S18535
18	110	3.1	384	9	S18535
17	110	3.1	384	9	S18535
16	110	3.1	384	9	S18535
15	110	3.1	384	9	S18535
14	110	3.1	384	9	S18535
13	110	3.1	384	9	S18535
12	110	3.1	384	9	S18535
11	110	3.1	384	9	S18535
10	110	3.1	384	9	S18535
9	110	3.1	384	9	S18535
8	110	3.1	384	9	S18535
7	110	3.1	384	9	S18535
6	110	3.1	384	9	S18535
5	110	3.1	384	9	S18535
4	110	3.1	384	9	S18535
3	110	3.1	384	9	S18535
2	110	3.1	384	9	S18535
1	110	3.1	384	9	S18535

ALIGNMENTS

RESULT	1
ENTRY	B33601
TITLE	lcrV protein - Yersinia pestis
ORGANISM	formal_name Yersinia pestis
DATE	17-Jan-1990 #sequence_revision 17-Jan-1990 #text-change 23-Mar-1993
ACCESSIONS	B33601
REFERENCE	A33601

#author Price, S.B.; Leng, K.Y.; Barve, S.S.; Straley, S.C.
#journal J. Bacteriol. (1989) 171:5646-5653
#title Molecular analysis of IcrGVH, the V antigen operon of
Yersinia pestis.
#cross-references MIMD:90008806
#accession B33601

```
SUMMARY      #length 326 #molecular-weight 37226 #checksum 6238
#cross-references GR:M26405
#residues    1-326 ##label PRI
#molecule_type DNA
#status      Preliminary
```

Query Match	63.3%	Score 2245	DB 9	Length 326
Best Local Similarity	99.45%	Pred. No. 9	45e-282	
Matches 324	Conservative	2	Mismatches 0	Indels 0
			Gaps 0	
Db	1	mlrayeqnqpfhiedlekvrveqltghgssvleelvglvkdknldisikypcrkdsvefa	60	
Qy	196	MIRAVEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVGLVMDKNIDISIKKDPKRDSEVFA	255	
Db	61	nrvtltdiellkkllyfipedaillkgghydnqngikrvkeflaesspnqtwelira fama	120	
Qy	256	NRVTIDIEILLKTLIAYFLPEDTLTKGGHYDNQNGIKRVKEFLAESSPNQWELIRAFMA	315	
Db	121	vmhfsftadridddvixkivdasmhbgdarskileelaetaelklysvigaeknhlss	180	
Qy	316	VMHFSFTADRIDDDILKIKYVDSMHHBGDARSKILEELAETAEIKLYSVIOAEINKHLSS	375	
Db	181	sgtinhbkslnhdnklgytdeeflkaaseyullkmpgttqvggsakkiyviskdfll	240	
Qy	376	SGTINHBSKSLNLDKNLYGTDEEFLKASAEYULLKMPGTTQLQVVGSEKKIYSINDFL	435	
Db	241	gsemrtcalanlnksysyndnneishfatscdskrpindlvsqgtitgdsitstrfns	300	
Qy	436	GSEMRTCALANLNKNSYSYNDDNNEISHFATCSDSKRPLNDLVYSQTTQLSDITSFNS	495	
Db	301	aiealnrfikqydvsmqgrllldtsegk	326	

|||||
OY 496 AIEALNRFIOKYDSVMORLLDPTSGK 521

RESULT 2
ENTRY B37314 #type complete
TITLE regulatory protein LcrV - Yersinia pseudotuberculosis
ORGANISM #formal_name Yersinia pseudotuberculosis
DATE 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 17-Feb-1994

ACCESSIONS B37314
REFERENCE A37314
#authors Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.;
#journal Maccellaro, A.; Baeckman, A.; Boelin, I.; Wolf-Watz, H.
#title J. Bacteriol. (1991) 173:1607-1616
Analysis of the V antigen lcrGVH-yopBD operon of Yersinia
pseudotuberculosis: evidence for a regulatory role of LcrV
and LcrV.

#accession B37314
#status Preliminary
#molecule_type DNA
#residues 1-326 #label BER
#cross-references GB:M57893

SUMMARY #length 326 #molecular-weight 37336 #checksum 4689

Query Match 61.8%; Score 2192; DB 9; Length 326;
Best Local Similarity 96.6%; Pred. No. 2,08e-274;
Matches 315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 1 mlrayerqpnqfiedlekvrveqlcgshsvleelvgqvkdknldlslydkpdksevf 60
OY 196 MIRAYEQNPQHFIEDLEKVRVEQLCGSHSVLEELVQLVKDKNDISIKYDPRKDSYV 255
Db 61 nrvitddellkklayflpedaalkgqydnqnglkrvveflseesntqwellrafna 120
OY 256 NKVITDDLELKLILAYFLPEDTILKGCHYDQNGIKRKRVEFESSPTQWELRAFNA 315
Db 121 vlfsltdridddllkvlvdsnmhgdarskireelaetlaeklysvgaelnkhss 180
OY 316 VWFSLTRDIDDDILKVLVDSNMHGDARSKIREELAEITLAEKLYSTVQLEFNKHSS 375
Db 161 gctlnhdkslnmcknljyvtdeefkasaeykilekmpqtllegeetekkivsknfl 240
OY 376 SGTINIHDKSIMLMDKNLYGTDEEFKASAEYKILEKMPQTITQVDSSEKIVSINDL 435
Db 241 esekrtgaglnkdsysynkshatccsdksrplndlvsgktqldstsrfs 300
OY 436 GSENRGTGALMKNSYSYKDNNELSHPATYCSKSRPLNDLVSOKTQLSDITSRFS 495
Db 301 alealnrfiqkydsymgrllddtsqk 326
OY 496 AIEALNRFIOKYDSVMORLLDPTSGK 521

RESULT 3
ENTRY S13008 #type complete
TITLE capsular antigen Fl precursor - Yersinia pestis
ORGANISM #formal_name Yersinia pestis
DATE 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
ACCESSIONS S13008; S23725
REFERENCE S13008
#authors Galyov, E.E.; Smirnov, O.Y.; Karlishhev, A.V.; Volkovoy, K.I.;
Denesyuk, A.I.; Nazimov, I.V.; Rubtsov, K.S.; Abramov,
V.M.; Dalvadganz, S.M.; Zav'yalov, V.P.
#journal FEBS Lett. (1990) 277:230-232
#title Nucleotide sequence of the Yersinia pestis gene encoding Fl
antigen and the primary structure of the protein. Putative
T and B cell epitopes.
#cross-references MUID:91099503
#accession S13008
#molecule_type DNA
#residues 1-170 #label GAL

##cross-references EMBL:X61996
GENETICS
#gene cafI
FEATURE 1-21
22-170
#domain signal sequence #status experimental #label SIG
#product capsular antigen Fl #status experimental #label
MAT

SUMMARY #length 170 #molecular-weight 17666 #checksum 5455

Query Match 31.0%; Score 1100; DB 9; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.88e-124;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkksvialaalfgtaanaadtlastratatlveparitlykekapitmdnqndt 60
OY 24 MKKISSVIAIALFGTIAANADLTASTATATLYEPARITLYTKEGAPITMDNGNDT 83
Db 61 ellvgtlcggkgtctsvnfdaagdpmylftsqdgnbqftkvlgkdsrdldis 120
OY 84 ELLVGTLLTGGVKTGTSTSVNFTDAAGDPMYLFTSQDGNHGFTRKVIKDSRDIS 143
Db 121 pkvngenvlgddvylatgsqdfivrsgskgkilaagkytdavtvsnq 170
OY 144 PKVNGENVLGDDVYLATGSQDFIVRSIGSKGKILAAGKYTDVAVTVSNQ 193

RESULT 4
ENTRY I58315 #type complete
TITLE WT1 - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1996

ACCESSIONS I58315
REFERENCE I58315
#authors Hamilton, T.B.; Barilla, K.C.; Romanjuk, P.J.
#journal Nucleic Acids Res. (1995) 23:277-284
#title High affinity binding sites for the Wt1ms' tumour suppressor
protein WT1.
#cross-references MUID:95166649
#accession I58315
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-168 #label RPS
##cross-references GB:S75264; NID:9896246; CDS_PID:9896247

GENETICS
#note gene name WT1
SUMMARY #length 168 #molecular-weight 20165 #checksum 6457

Query Match 4.7%; Score 168; DB 13; Length 168;
Best Local Similarity 66.7%; Pred. No. 4.08e-05;
Matches 20; Conservative 7; Mismatches 1; Indels 2; Gaps 1;

Db 1 mgbbhhhhhhshleg--rhmrtygv 28
OY 1 MGHNNHHHHHSHGHIDDDDKMKKISSV 30

RESULT 5
ENTRY S07904 #type complete
TITLE CS3 pilin precursor - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

ACCESSIONS S07904
REFERENCE S07904
#authors Jajajakumar, M.B.; Thomas, C.J.; Halter, R.; Manning, P.A.
#journal Mol. Microbiol. (1989) 3:1685-1695
#title Genes for biosynthesis and assembly of CS3 pilin of CFA/II
enterotoxigenic Escherichia coli: novel regulation of pilus
production by bypassing an amber codon.
#cross-references MUID:90158116
#accession S07904
#status Preliminary

##molecule-type DNA
##residues 1-168 ##label JAL
##cross-references EMBL:X16944
SUMMARY #length 168 #molecular-weight 17491 #checksum 8973

Query Match 3.6%; Score 127; DB 9; Length 168;
Best Local Similarity 24.1%; Pred. No. 3,73e-01;
Matches 41; Conservative 47; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlkiky11g1samsyslaaagpllkela1nvspaaladatwapqdn1lsntg-v 59
| | | | | : : : : : | | | : : : : : | : : : : :
24 MKRISV-IAIALFGRIA-TANADLFASTATATVEPARITLYKEGAPITMDNGNI 81
| | | | | : : : : : | | | : : : : : | : : : : :
Db 60 -sntlvgvltlntsidsivtsastvsdskngt-vlfahetnsasfalc-istdani 116
| | | | | : : : : : | | | : : : : : | : : : : :
82 DFLLVGLTGLGKYKTGTS-TSVNFTDAAGDPMYLFTFSQDNNHOFYTKVIGKDSRDF 140
| | | | | : : : : : | | | : : : : : | : : : : :
Db 117 tld-knagntiv-ktngsqplnplkfttgnegnhlvsngnyranitlt 164
| | | | | : : : : : | | | : : : : : | : : : : :
QY 141 DISPKVNGENLVGDVYLVATGSODFEVRSIGSKGK-LAAGKTYDAVT 189
| | | | | : : : : : | | | : : : : : | : : : : :
RESULT 6
ENTRY S57382 #type complete
TITLE hypothetical protein YOL087c - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES hypothetical protein O0944
ORGANISM formal_name Saccharomyces cerevisiae
DATE 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 02-Aug-1996
ACCESSIONS S57382; S66781; S50418
REFERENCE S57374
#authors Zumbstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
#journal Yeast (1995) 11:975-986
#title A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.
#accession S57382
#status nucleic acid sequence not shown
##molecule-type DNA
##residues 1-1116 ##label ZUM
##cross-references EMBL:X83121
REFERENCE S66775
#authors Zumbstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
#submission submitted to the Protein Sequence Database, July 1996
#accession S66781
##molecule-type DNA
##residues 1-1116 ##label ZUM
##cross-references EMBL:Z74829
##experimental_source strain S28C
GENETICS
#map-position 15L
SUMMARY #length 1116 #molecular-weight 125381 #checksum 1996

Query Match 3.6%; Score 127; DB 11; Length 1116;
Best Local Similarity 47.1%; Pred. No. 3,73e-01;
Matches 16; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Db 365 hhhhhheegnistdtkvkkyygildal1 398
| | | | | : : : : : | | | : : : : : | : : : : :
QY 3 HHHHHHHHSSGSHDDDKMKRISVIAIALF 36
| | | | | : : : : : | | | : : : : : | : : : : :
RESULT 7
ENTRY A34952 #type complete
TITLE CS3 fimbrial protein precursor - Escherichia coli
ORGANISM formal_name Escherichia coli
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 04-Nov-1994
ACCESSIONS A34952
REFERENCE A34952

#authors Boylan, M.; Smyth, C.J.; Scott, J.R.
#journal Infect. Immun. (1988) 56:3297-3300
#title Nucleotide sequence of the gene encoding the major subunit of CS3 fimbriae of enterotoxigenic Escherichia coli.
#cross-references MIMD:89032631
#accession A34952
##molecule-type DNA
##residues 1-168 ##label BOY
##cross-references GB:M35657
FEATURE
1-15 #domain (or 1-22) signal sequence #status predicted
16-168 #label SIG\ #product (or 17-168) CS3 fimbrial protein #status predicted #label MAT
SUMMARY #length 168 #molecular-weight 17464 #checksum 9103

Query Match 3.5%; Score 123; DB 9; Length 168;
Best Local Similarity 23.5%; Pred. No. 8.48e-01;
Matches 40; Conservative 48; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlkiky11g1samsyslaaagpllkela1nvspaaladatwapqdn1lsntg-v 59
| | | | | : : : : : | | | : : : : : | : : : : :
QY 24 MKRISV-IAIALFGRIA-TANADLFASTATATVEPARITLYKEGAPITMDNGNI 81
| | | | | : : : : : | | | : : : : : | : : : : :
Db 60 -sntlvgvltlntsidsivtsastvsdskngt-vlfahetnsasfalc-istdani 116
| | | | | : : : : : | | | : : : : : | : : : : :
QY 82 DFLLVGLTGLGKYKTGTS-TSVNFTDAAGDPMYLFTFSQDNNHOFYTKVIGKDSRDF 140
| | | | | : : : : : | | | : : : : : | : : : : :
Db 117 tld-knagntiv-ktngsqplnplkfttgnegnhlvsngnyranitlt 164
| | | | | : : : : : | | | : : : : : | : : : : :
QY 141 DISPKVNGENLVGDVYLVATGSODFEVRSIGSKGK-LAAGKTYDAVT 189
| | | | | : : : : : | | | : : : : : | : : : : :
RESULT 8
ENTRY S47608 #type complete
TITLE actin homolog YOL081c - yeast (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein J1012; protein YOL081c
ORGANISM formal_name Saccharomyces cerevisiae
DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 08-Sep-1995
ACCESSIONS S47608; S56029; S56858; S37563
REFERENCE S47608
#authors Wintersberger, U.
#submission submitted to the EMBL Data Library, December 1993
#accession S47608
##molecule-type DNA
##residues 1-489 ##label WIN
##cross-references EMBL:X75317
REFERENCE S56016
#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Chaiwatzis, N.; Baur, A.; Boles, E.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Zimmermann, F.K.
#journal Yeast (1995) 11:681-689
#title Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)(2)-Cys(6) binuclear cluster domain and a putative alpha-2-SCB-alpha-2 binding site.
#accession S56029
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-489 ##label MIO
##cross-references EMBL:X83502
#note the nucleotide sequence was submitted to the EMBL Data Library, December 1994
REFERENCE S56855
#authors Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chaiwatzis, N.; Fournier, C.; Schmitt, S.; Velten, C.; Wilhelm, N.; Witzel, A.; Zimmermann, F.K.
#submission submitted to the Protein Sequence Database, September 1995
#accession S56858
##molecule-type DNA
#residues 1-489 ##label MIW

GENETICS		#cross-references EMBL:749356	
#gene	ACT3		
#map_position	10L		
CLASSIFICATION	#superfamily actin		
SUMMARY	#length 489 #molecular-weight 54831 #checksum 8019		
Query Match 3.5%; Score 123; DB 7; Length 489;			
Best Local Similarity 25.8%; Pred. NO. 8,48e-01;			
Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;			
Db	22 gsytnigysddefpsilpsvgykytadegnkklfsesqsigidprkdyelkplie-nglv 80		
Oy	93 GGYKGTSTSTVNFDAAGDPMLTLFTSODNNNOFTKTVIGKDSRDPDISPKVNGENLV 152		
Db	81 id 82		
Oy	153 GD 154		
RESULT	9		
ENTRY	S33821	#type complete	
TITLE	median body protein - Giardia lamblia		
ORGANISM	#formal name Giardia lamblia		
DATE	06-Jan-1995	#sequence_revision 06-Jan-1995	#text_change
ACCESSIONS	S33821		
REFERENCE	S33821		
#authors	Marshall, J.; Holberton, D.V.		
#journal	J. Mol. Biol. (1993) 231:521-530		
#title	Sequence and structure of a new coiled coil protein from a microtubule bundle in Giardia.		
#accession	S33821		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-857	#label MAR	
#cross-references	EMBL:X64517		
SUMMARY	#length 857 #molecular-weight 100583 #checksum 6805		
Query Match 3.5%; Score 124; DB 12; Length 857;			
Best Local Similarity 20.1%; Pred. NO. 6,92e-01;			
Matches 43; Conservative 71; Mismatches 82; Indels 18; Gaps 17;			
Db	582 erwveerlqkeennllkqritelegqqrtaivretemsalrekaneldgyntergareh 641		
Oy	205 OHFIED-LEKRVVEQLTGSSVLELQVLYKDRNIDISIKYDPRKSEVFA-NRVTYD- 261		
Db	642 eimmlrkdalesdklqgnrvmamel-telrekyqlleklyqekrrardvemlelrhamd 700		
Oy	262 DIELK-KILVYF-PREPTILKGHYNDQNLNGIKRV-K-ELLESSPTQ-WEURA-FMA 315		
Db	701 vdtlveeqrllemlraeiklvmyndqadkarlqeqlekmskliefemimdd-prrl 759		
Oy	316 VMHFEFLADRIDDDI--LKAVYDSNNHHGDARSKRRELALTLMLKITYSQAIFIKHL 373		
Db	760 klqvk-eeldlktan-mek-lyeeykkledqlkat 790		
Oy	374 SSSGTINIHDKSINIMDKNLVG-YTD-ELIRKAS 405		
RESULT	10		
ENTRY	S15999	#type complete	
TITLE	faty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast		
ORGANISM	(Yarrowia lipolytica)		
DATE	#formal name Yarrowia lipolytica, Candida lipolytica		
ACCESSIONS	30-Jun-1992	#sequence_revision 30-Jun-1992	#text_change
REFERENCE	11-Jun-1993		
#authors	S15999		
#journal	Koetting, H.; Rotner, G.; Beck, K.F.; Schweizer, M.;		
#title	Schweizer, E.		
	Mol. Gen. Genet. (1991) 226:310-314		
	The pentafunctional FAS1 genes of Saccharomyces cerevisiae		

[illegible]

! :
QY 158 LATGSODFFV 167

Search completed: Fri Apr 25 12:04:07 1997
Job time : 83 secs.

Db 241 gsenkrtgajnlknsysynkdmelshfatcsdksrplndlvsgktqlsdtsrfs 300
 OY 436 GSENRKRGALGKNSYSYNKDNNELSHFATCSDKSRPLNDLVSGKTTQLSDTSRFS 495
 Db 301 aiealnrfikkydsvmqrllldtsgk 326
 OY 496 AIEALNRFIOKYSVMQRLLDTSCK 521

RESULT 2
 ID LCRY_YERPS STANDARD: PRT: 326 AA.
 AC P23994:

DT 01-MAR-1992 (REL. 21, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
 DE VIRULENCE-ASSOCIATED V ANTIGEN (LOW CALCIUM RESPONSE LOCUS PROTEIN V).
 GN LCRY.
 OS YERSINIA PSEUDOTUBERCULOSIS.
 CC PLASMID P1B1.
 CC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 CC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YPIII;
 RX MEDLINE: 91154114.
 RA BERGMAN T., HAKANSSON S., FORSBERG A., NORLANDER L., MACCELLARO A.,
 RL J. BACTERIOL. 173:1607-1616(1991).
 CC -I- FUNCTION: INVOLVED IN CA(2+) REGULATION OF YOP EXPRESSION, WHICH
 CC INCLUDES THE EXPORT PROCESS.
 CC -I- SUBCELLULAR LOCATION: SECRETED.
 DR EMBL: M57893: G155458; -.
 DR PIR: B37314; B37314.
 KW PLASMID; ANTIGEN; VIRULENCE.
 SQ SEQUENCE 326 AA; 37336 MM; 7D84E243 CRC32;

Query Match 61.8%; Score 2192; DB 5; Length 326;
 Best Local Similarity 96.6%; Pred. No. 0.00e+00;
 Matches 315; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 1 mirayegnpqhfieldekrrveqlgshssvleelwqlvkdknidslkydprkdsvefa 60
 OY 196 MIRAEQNPQHFIEDLEKRRVEQLGSHSSVLEELVQLVKDNIDISIKYDPRKDSVEFA 255
 Db 61 nrvtddlellkkllyayfipedaalkgghyngngikrvkeflsspnrtwelfatma 120
 OY 256 NRVIDDIELLKKILAYFLPEDTILKGHYDNQNGIKRVKEFLSSPNRTWELRAFMA 315
 Db 121 vihfaletdriddllkviydsmbhgdarcklreelaetelklyavtgeinkhlis 180
 OY 316 VIMHSELVDRIDDDILKVIYDSMBHGDARSKLREELAELELTKLYSYIOEINKHLIS 375
 Db 181 ggtlnihkkslnlmknllysydeefikasaeykillekmpgttisegetekelkvsiknfl 240
 OY 376 SGTINIHKKSILMKNLKYGYDEDEFKASAEYKILLEKMPGTTIYVDSSEKKIVSIKDFL 435
 Db 241 esekrtgajnlknsysynkdmelshfatcsdksrplndlvsgktqlsdtsrfs 300
 OY 436 GSENRKRGALGKNSYSYNKDNNELSHFATCSDKSRPLNDLVSGKTTQLSDTSRFS 495
 Db 301 aiealnrfikkydsvmqrllldtsgk 326
 OY 496 AIEALNRFIOKYSVMQRLLDTSCK 521

RESULT 3
 ID CARL_YERPE STANDARD: PRT: 170 AA.
 AC P26948:
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)

DE F1 CAPSULE ANTIGEN PRECURSOR.
 GN CARL.
 OS YERSINIA PESTIS.
 CC PLASMID PERA.
 CC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 CC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91099503.
 RA GALYOV E.E., SMIRNOV O.Y., KARLISHEV A.V., VOLKOVOY K.I.,
 RA DENESYUK A.I., NAZIMOV I.V., RUBTSOV K.S., ABRAMOV V.M.,
 RA DALVADYANZ S.M., ZAV'YALOV V.P.;
 RL FEBS LETT. 277:230-232(1990).
 CC -I- SUBCELLULAR LOCATION: CAPSULE.
 DR EMBL: X61996: G48621; -.
 DR PIR: S13008; S13008.
 KW PLASMID; SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 170 F1 CAPSULE ANTIGEN.
 FT DOMAIN 100 150 CONTAINS POTENTIAL ANTIGENIC DETERMINANTS
 FT THAT MAY STIMULATE T-CELLS.
 SQ SEQUENCE 170 AA; 17666 MM; 354322B5 CRC32;

Query Match 31.0%; Score 1100; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 1.64e-160;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mkkssvialalfgrtanaadltastatatlvepartltykagaprlmdngndt 60
 OY 24 MKKISSVIALALFGRTANADLTASTATATVLEPARITLYKKGAPRTIMNGNDT 83
 Db 61 ellvgtcllggktytstsvnficaagdpmylftsgdgnhftkvtjgkdsrfdais 120
 OY 84 ELLVGTCLLGCKTGTSTSVNFTDAADPMYLFFTSGDGNHFTKVTJGKDSRFDIPS 143
 Db 121 pkvgenlvgdvvlatsgqdfivrslysgkagklaagkytclavtvsng 170
 OY 144 PKVGENLVGDVVLATSGQDFIVRSISGKGLAAGKYTCLAVTVVSNG 193

RESULT 4
 ID FMS3_ECOLI STANDARD: PRT: 168 AA.
 AC P15488:
 DT 01-APR-1990 (REL. 14, CREATED)
 DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CS3 FIMBRIAL SUBUNIT A PRECURSOR (CS3 PILIN).
 OS ESCHERICHIA COLI.
 CC PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
 CC ENTEROBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-52.
 RC STRAIN-PB176;
 RX MEDLINE: 90158116.
 RA JALAJUKUMARI M.B., THOMAS C.J., HALTER R., MANNING P.A.;
 RL MOL. MICROBIOL. 3:1685-1695(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89032631.
 RA BOYLAN M., SMYTH C.J., SCOTT J.R.;
 RL INFECT. IMMUN. 56:3297-3300(1988).
 RN [3]
 RP SEQUENCE OF 23-45.
 RC STRAIN-E9034A;
 RX MEDLINE: 90036735.
 RA HALL R.H., MANEVAL D.R. JR., COLLINS J.H., THEIBERT J.L.,
 RA LEVINE M.M.;
 RL J. BACTERIOL. 171:6372-6374(1989).
 CC -I- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
 CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
 CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
 CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
 DR EMBL: X16944; G41161; -.

DR EMBL: M35657; G145627; -
DR PIR: A34952; A34952.
DR FIMBRIA; SIGNAL.
KW FIMBRIA; SIGNAL.
FT SIGNAL 1 22 CS3 FIMBRIAL SUBUNIT A.
FT CHAIN 23 168 N -> S (IN REF. 2).
FT CONFLICT 83 83
SQ SEQUENCE 168 AA; 17491 MW; 4D5CD89A CRC32.

Query Match 3.68; Score 127; DB 4; Length 168;
Best Local Similarity 24.18; Pred. No. 3.28e-02;
Matches 41; Conservative 47; Mismatches 72; Indels 10; Gaps 10;

Db 1 mlklylllglsamsyslaaagplltkelalnvspaladepqnlstntg-v 59
QY 24 MKRISSV-LAIALFGLTA-TANADLTASTATATAVEPARITLYTREGAPITMDNGT 81

Db 60 -snltvgvltlntsltdtvsiaastnvsdtkngt-vtfahetnsaafatt-1stdnanl 116
QY 82 DTELIVGTTLTGKVKCTTS-TSVNFTDAAGDPWYLTFTSGDGNHGFITKVKIGKSDRF 140

Db 117 tld-knagntiv-ktngsqipnlplklttegnehlvsngnyranltit 164
QY 141 DISPKVNGENLVGDVVLATGSDFEVRSIGSKGK-LAAGKYTDVAVT 189

RESULT 5
ID ACT3_YEAST STANDARD; PRT; 489 AA.
AC P80428;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE ACTIN-LIKE PROTEIN ACT3.
GN ACT3 OR YJL081C OR J1012.
OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94336725.
RA HARATA M., KARWAN A., WINTERSBERGER U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 91:8258-8262(1994).
RN [2]
RP ERRATUM.
RX MEDLINE; 95024194.
RA HARATA M., KARWAN A., WINTERSBERGER U.;
RL PROC. NATL. ACAD. SCI. U.S.A. 91:10757-10757(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C;
RX MEDLINE; 96093911.
RA MIOSGA T., SCHAFF-GERSTENSCHLAGER I., CHALWATZIS N., BAUR A.,
RA BOLES E., FOURNIER C., SCHMITT S., VELTEN C., WILHELM N.,
RA ZIMMERMANN F.K.;
RL YEAST 11:681-689(1995).
CC -I- SIMILARITY: TO ACTIN. STRONG, TO OTHER ACTIN-LIKE PROTEINS
OF THE ARP4 SUBFAMILY.
CC EMBL; X75317; G436808; -
DR EMBL; X83502; G929875; -
DR EMBL; Z49356; G1008244; -
DR PIR; S47608; S47608.
DR LISTA; SC01441; ACT3.
DR SGD; L0000027; ACT3.
DR PROSITE; PS01132; ACTINS_ACT_LINE.
KW STRUCTURAL PROTEIN; CYTOSKELETON.
SQ SEQUENCE 489 AA; 54831 MW; C41435B1 CRC32.

Query Match 3.58; Score 123; DB 1; Length 489;
Best Local Similarity 25.88; Pred. No. 9.09e-02;
Matches 16; Conservative 21; Mismatches 24; Indels 1; Gaps 1;

Db 22 gsytltnygsdfigslpsvygkytadgnkklfsegsjprkdvklplle-ogly 80
QY 93 GGKTKTSTSVNFTDAGDPWYLTFTSGDGNHGFITKVKIGKSDRFDISPKVNGENLV 152

Db 81 id 82
QY 153 GD 154

RESULT 6
ID MEDB_GITALA STANDARD; PRT; 857 AA.
AC Q08014;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE MEDIAN BODY PROTEIN.
OS GIARDIA LAMBLA (GIARDIA INTESTINALIS).
OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
OC HEXAMITIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PORTLAND-1;
RX MEDLINE; 93287123.
RA MARSHALL J., HOLBERTON D.V.;
RL J. MOL. BIOL. 231:521-530(1993).
CC -I- FUNCTION: MAY HAVE A ROLE IN IMMOBILISING THE MICROTUBULES
BETWEEN CELL DIVISIONS.
CC -I- SUBCELLULAR LOCATION: MEDIAN BODY.
CC -I- DOMAIN: SHOWS AN ALPHA-HELICAL COILED COIL STRUCTURE (30
REPEATING HEPTADS).
DR EMBL; X64517; G312671; -
KW CYTOSKELETON; MICROTUBULES; COILED COIL; HEPTAD REPEAT PATTERN.
SQ SEQUENCE 857 AA; 100583 MW; 5E2BBA84 CRC32.

Query Match 3.58; Score 124; DB 6; Length 857;
Best Local Similarity 20.18; Pred. No. 7.06e-02;
Matches 43; Conservative 71; Mismatches 82; Indels 18; Gaps 17;

Db 582 ervveerickckenllkqptlelegqratvretemalrekaneldgynreargen 641
QY 205 QHTEED-LEKRVVEQLTGHOSSVLEEVOLVKRNIDISIKIDPRKDFEFA-NRYITD- 261

Db 642 elmlldkalesdklrgdnrvamel-telrekvllleklyekardveamlrlpkamd 700
QY 262 DIELK-KILAYF-LPEDITLKGGHNDQNGIKRV-K-EFLSSPNQ-WELRA-FWA 315

Db 701 vdtlveekgrlemrlaelklkvnnyqjadakarlegqklesdklliefemlnd-nrrl 759
QY 316 VMHFSLTADRIDDI--LKVIYDSNMNHGDPARSKREELAEITAEIKTYSVIOAEIKHL 373

Db 760 klqkv-elldktan-mek-lyeeykkledqlkat 790
QY 374 SSSGTTIHDKSINLMDKNLYG-YTD-EELFKAS 405

RESULT 7
ID PAS1_YARLI STANDARD; PRT; 2076 AA.
AC P34229;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE FATY ACID SYNTHASE, SUBUNIT BETA (EC 2.3.1.86) (CONTAINS: 3-
DE HYDROXYPALMITOYL-[ACYL-CARRIER-PROTEIN] DEHYDRATASE (EC 4.2.1.61);
DE ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADH) (EC 1.3.1.9); [ACYL-
DE CARRIER-PROTEIN] ACETYLTRANSFERASE (EC 2.3.1.38); [ACYL-CARRIER-
DE PROTEIN] MALONYLTRANSFERASE (EC 2.3.1.39); AND S-ACYL FATY ACID
DE SYNTHASE THIOESTERASE (EC 3.1.2.14)).
GN PAS1.
OS YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CX 161-1 B ADEL A;
RX MEDLINE; 91238709.
RA KOETIG H., ROTTNER G., BECK K.-F., SCHWEIZER M., SCHWEIZER E.;
RL MOL. GEN. GENET. 226:310-314(1991).

CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
CC THE BETA SUBUNIT CONTAINS DOMAINS FOR: [ACYL-CARRIER PROTEIN]
CC ACETYLTRANSFERASE AND MALONYLTRANSFERASE, S-ACYL FATTY ACID
CC SYNTHASE THIOESTERASE, ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND
CC 3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE.
CC -1- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+) +
CC CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADPH =
CC LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+) +
CC CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA
CC + ACETYL-[ACYL-CARRIER PROTEIN].
CC -1- CATALYTIC ACTIVITY: MALONYL-COA + [ACYL-CARRIER PROTEIN] = COA
CC + MALONYL-[ACYL-CARRIER PROTEIN].
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN]
CC = 2-HEADCENOL-[ACYL-CARRIER PROTEIN] + H(2)O.
CC -1- CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NAD(+) = 2,3-
CC DEHYDROACYL-[ACYL-CARRIER PROTEIN] + NADH.
CC -1- CATALYTIC ACTIVITY: OLEOYL-[ACYL-CARRIER PROTEIN] + NAD(+) =
CC ACYL-CARRIER PROTEIN + OLEATE.
CC -1- SUBUNIT: FATTY ACID SYNTHETASE ARE [ALPHA(6)BETA(6)] HEXAMERS OF
CC TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
CC EMBL: X59690; G297853; -.
DR PIR: S15999; S15999.
DR FATTY ACID BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME; OXIDOREDUCTASE;
KM TRANSFERASE; HYDROLASE; LIGASE; NAD: NADP.
FT DOMAIN 1 470 ACETYL TRANSFERASE.
FT DOMAIN 482 869 ENOYL REDUCTASE.
FT DOMAIN 1186 1647 DEHYDRATASE.
FT DOMAIN 1648 1869 MALONYL/PALMITOYL TRANSFERASE.
FT ACT_SITE 276 276 ACETYL TRANSFERASE (BY SIMILARITY).
FT ACT_SITE 1832 1832 MALONYLTRANSFERASE (BY SIMILARITY).
SQ SEQUENCE 2076 AA; 230223 MW; E10A5234 CRC32;

Query Match 3.5%; Score 123; DB 3; Length 2076;
Best Local Similarity 31.3%; Pred. No. 9,09e-02;
Matches 25; Conservative 22; Mismatches 28; Indels 5; Gaps 5;

Db 1266 tdnrttrkfeiykylfggsk-feldtdlt-eeliggddtlsgkaladtvhvngkgeaf 1325
OY 119 TSQDGNHGHFTTKV-IGKSRDPDISPKNGENLVGDVLAATGSDPFRSISGKGKL 177
DB 1326 v-gistsagtv-fapmdfal 1343
OY 178 AAGXYTDAVTAVTSNOEFMI 197

RESULT 8
AC P40555; STANDARD: PRT; 220 AA.
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 24.8 KD PROTEIN IN FAA3-BET1 INTERGENIC REGION.
GN Y11007C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA BARRELL B.G., BADCOCK K., BANKIER A.T., BOWMAN S., BROWN D.,
RA CHURCHER C.M., CONNOR R., COPSEY T., DEAR S., DEVLIN K., FRASER A.,
RA GENTLES S., HAMLIN N., HORSNELL T.S., HUNT S., JAGELS K., JONES M.,
RA LOUIS E., LYE G., MOULE S., MOULE T., ODELL C., PEARSON D.,
RA RAUNDSEAM M.A., RILES L., ROWLEY N., SKELTON J., SMITH V.,
RA WALSH S.V., WHITEHEAD S.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z38113; G558397; -.
DR EMBL: Z47047; G763339; -.
DR PIR: S48450; S48450.
KM HYPOTHEICAL PROTEIN.
SQ SEQUENCE 220 AA; 24846 MW; B3911075 CRC32;

Query Match 3.4%; Score 120; DB 11; Length 220;
Best Local Similarity 22.8%; Pred. No. 1,93e-01;
Matches 34; Conservative 39; Mismatches 69; Indels 7; Gaps 7;

Db 38 ktditqleay-fsvlegq-igmbsalvtpdy-prsdvdlqvtmkrkvnm[knd]n 94
OY 213 KVRVE-QLTGHSSVLEELVOLVKKNDISIKYPRKDSFEVFAFNVITDDIELKKILA 271
DB 95 hllqshvylngfhfmmvknsgdarrn-nddgaqyilpafissevpgpsdkaiky 153
OY 272 YLPEDTILKGGHYNOJONGIKRKVERFLESSPNTOWELR-AFMAVHPSLADRIDDI 330
DB 154 ddklislgnvhaanbsklqnlqmvwmkne 182
OY 331 LKVIYDSNMHHGDASKLRE-ELAEITAE 358

RESULT 9
AC P25332; STANDARD: PRT; 333 AA.
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE PROBABLE RIBOKINASE (EC 2.7.1.15).
GN RBK1 OR YCR36W OR YCR523.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE: 91181345.
RA THERREY A., FAIRHEAD C., DUJON B.;
RL YEAST 6:521-534(1990).
CC -1- CATALYTIC ACTIVITY: ATP + D-RIBOSE = ADP + D-RIBOSE 5-PHOSPHATE.
CC -1- PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
CC -1- SIMILARITY: BELONGS TO A FAMILY OF CARBOHYDRATE KINASES THAT
CC GROUPS TOGETHERS PERK, FRUK, GSK, IACC, RSK, AND SCRK.
DR EMBL: X59720; E264378; -.
DR EMBL: X59720; E264378; -.
DR PIR: S12918; KIBYRB.
DR LISTA; SC00940; RBK1.
DR SGD; L0001587; RBK1.
DR PROSITE; PS00583; PERK_KINASES_1.
DR PROSITE; PS00584; PERK_KINASES_2.
KM TRANSFERASE; KINASE.
SQ SEQUENCE 333 AA; 36984 MW; 3E1772EC CRC32;

Query Match 3.4%; Score 120; DB 8; Length 333;
Best Local Similarity 23.2%; Pred. No. 1,93e-01;
Matches 22; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

Db 235 klmmkrrgylvmlgsrgvlfcshepsvqfipaigvsvvdtgagdtlglvltly 294
OY 176 KLAAGXYTDAVTAVTSNOEFMIRAYEQNHFIEDLEKRVLEOLTGHSSVLEELV-OLV 234
DB 295 ggetlsmalkfstlassltlqrgaaesmplykdv 329
OY 235 KDKNIDISIKIDPRKDSFEVFAFNVITDDIELKKI 269

RESULT 10
AC P32497; STANDARD: PRT; 812 AA.
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE NUCLEAR TRANSPORT PROTEIN NIP1.
GN NIP1 OR YMR309C OR YMR924.01C OR YMR952.11C.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93066237.

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RA GU 2., MOERSCHHELL R.P., SHERMAN F., GOLDFARB D.S.;
RL PROC. NATL. ACAD. SCI. U.S.A. 89:10355-10359(1992).
RN [12]
RP SEQUENCE OF 1-602 FROM N.A.
RC STRAIN-S288C / AB972.
RA CHURCHER C.M., LOUIS E.J., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [13]
RP SEQUENCE OF 571-812 FROM N.A.
RC STRAIN-S288C / AB972.
RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: INVOLVED IN TRANSPORT OF PROTEINS TO THE NUCLEUS;
CC PROBABLY VIA ITS SERINE-RICH ACIDIC N-TERMINAL.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC; MAINLY.
DR EMBL; L02889; -. NOT_ANNOTATED_CDS.
DR EMBL; 254141; G984682; -.
DR EMBL; 249212; G798951; -.
DR PIR; A46417; A46417.
DR LISTA; SC00714; NIP1.
DR SGD; L0001252; NIP1.
KW TRANSPORT; PROTEIN TRANSPORT.
FT DOMAIN 15 147 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 15 36 SER-RICH.
FT CONFLICT 111 111 V -> D (IN REF. 1).
FT CONFLICT 583 583 Q -> H (IN REF. 1).
FT CONFLICT 641 641 K -> N (IN REF. 1).
FT CONFLICT 643 643 K -> N (IN REF. 1).
SQ SEQUENCE 812 AA; 93204 MW; 4793DCE CRC32;

Query Match 3.2%; Score 115; DB 6; Length 812;
Best Local Similarity 29.2%; Pred. No. 6,54e-01;
Matches 31; Conservative 28; Mismatches 39; Indels 8; Gaps 8;

Db 700 wallpmetvlnslt-erygveslkyffsfkrfysfsvaki-aelfdl-penkkyevl 756
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 308 WELRAAMAMHFSLTDRDDDLKTYVDSNMH-HGD-ARSKIRELAETALAKTYVI 365
757 gsvia-eleipakln-dektlfvvekqdeltkleeamvlnkyki 800
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 366 QAEINKHLSSSGTINHDKSINLMRK-NLYGTDEIEIFASAYKI 410

RESULT 11
ID CDBP_YEAST STANDARD: PRT; 973 AA.
AC P41810;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DE COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).
GN SEC26.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-RS1255;
RX MEDLINE; 95014199.
RA DUDEN R., HOSOBUCHI M., HAMAMOTO S., WINEY M., BYERS B., SCHEKMAN R.;
RL J. BIOL. CHEM. 269:24486-24495(1994).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT
CC REVERSLY ASSOCIATES WITH GOLGI MEMBRANES TO FORM VESICLES THAT
CC MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI
CC UP TO THE TRANS GOLDI NETWORK. THE COATOMER COMPLEX IS REQUIRED
CC FOR BUDDING FROM GOLGI MEMBRANES.
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN ASSOCIATED WITH
CC NON-CLATHRIN COATED VESICLES AND CISTERNAE OF THE GOLGI COMPLEX,
CC BUT EXISTS ALSO AS A SOLUBLE CYTOSOLIC COMPLEX. THE EQUILIBRIUM
CC BETWEEN THOSE TWO FORMS MAY BE REGULATED BY GTP, ATP, OR BETA-COP
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: THE N-TERMINAL IS BLOCKED.

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CC -1- SIMILARITY: SIGNIFICANT, OF THE N-TERMINAL HALF OF BETA-COP WITH
CC THOSE OF BETA-ADAPTINS.
DR EMBL; U11236; G595413; -.
DR LISTA; SC01433; SEC26.
DR SGD; L0001847; SEC26.
KW TRANSPORT; PROTEIN TRANSPORT; GOLGI STACK; MEMBRANE; PHOSPHORYLATION.
SQ SEQUENCE 973 AA; 109033 MW; 75741C55 CRC32;

Query Match 3.2%; Score 112; DB 2; Length 973;
Best Local Similarity 20.3%; Pred. No. 1,34e+00;
Matches 31; Conservative 53; Mismatches 61; Indels 8; Gaps 8;

Db 307 rfgdnnanvgaeeitdlrvlaeqldvyskaldismdatsrnaedvqllkkelq 366
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 215 RVEQLTGHSVLEEL-VOLVADKNI-DISKYDPRKS-EFARVYTTDIELKTLIA 271
367 ttvnpddkqamyrqllklrtvavnfveamsvsllldfigelh-svaasgila-f 424
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 272 YLPEDTLKGGHYDNOQNGIKRVK-EFLSSPTWELRAFMAVMHFSLTADRIDD 330
425 lkeviekypqlaanllemvqtlkdvrsa-kay 456
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 331 LKVIYDSNMH-HGDARSKIRELAETALAKTY 362

RESULT 12
ID HA34_BRELK STANDARD: PRT; 173 AA.
AC Q99074;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE HAM34 PROTEIN.
GN HAM34.
OS BREXIA LACTUCAE (LETTUCE DOWNY MILDW).
OC EUKARYOTA; FUNGI; MASTIGOMYCOTINA; COMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-REBEL; TISSUE-SPORE;
RX MEDLINE; 92033077.
RA JUDELSON H.S., MICHELMORE R.W.;
RL MOL. PLANT MICROBE INTERACT. 3:225-232(1990).
CC -1- FUNCTION: COULD BE A STRUCTURAL PROTEIN REQUIRED FOR THE
CC INFECTION PROCESS OF B. LACTUCAE.
CC -1- TISSUE SPECIFICITY: GERMINATING SPORES.
DR EMBL; X16984; G2488; -.
KW SPORULATION; STRUCTURAL PROTEIN.
SQ SEQUENCE 173 AA; 16478 MW; 43864282 CRC32;

Query Match 3.1%; Score 109; DB 4; Length 173;
Best Local Similarity 24.3%; Pred. No. 2,70e+00;
Matches 28; Conservative 28; Mismatches 58; Indels 1; Gaps 1;

Db 1 mfsqdlvlaavaasqdaaptdattpaatttttttttttttttttttttttttttt 60
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 25 KTISSVIAALFGTITATAADLTASTATATLVLPARTTLTKGAPITIMDNGNIDE 84
61 ttaqpeaagatngtttppadgtqatapidataeesaagmptv-gldtsd 114
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 85 LVGVTLTGXYTGTSTSVNFTDAAGPMVLTFTSQDNNHGFYTKVIGKDSRD 139

RESULT 13
ID GIAC_GIALA STANDARD: PRT; 311 AA.
AC P38413;
DT 01-OCT-1994 (REL. 30, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DE GIARDIN GAMMA CHAIN.
OS GIARDIA LAMBLLA (GIARDIA INTESTINALIS).
OC EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA; MASTIGOPHORA; DIPLOMONADIDA;
CC HEXAMITIDAE.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 145-156.

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[illegible][illegible]

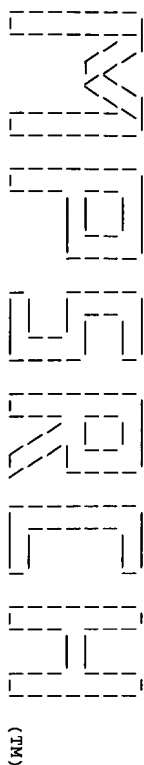
Mon Apr 28 07:53:52 1997

US-08-699-716A-2.rsp

Page 7

OY 362 YSVIOAEINKHLSSGTHNI 381

Search completed: Fri Apr 25 12:02:27 1997
job time : 52 secs.



(TM)

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MPern_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Apr 25 18:31:48 1997; Maspar time 1301.65 Seconds
1337.742 Million cell updates/sec

Tabular output not generated.

Title: >US-08-699-716A-1
Description: (1-1566) from US08699716A.seq
Perfect Score: 1566
N.A. Sequence: 1 ATGGCCGATCATCATCATCA.....ATGACACGCTGTGTAATGA 1566
Comp: TACCCCGTAGTAGTACTACT.....TACTGTGACAGACATTACT

Scoring table: TABLE default
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

emb1-new11
1: BCT 2: FUN 3: GEN 4: HUM1 5: HUM2 6: HUM3 7: INV1 8: INV2
9: INV3 10: INV4 11: INV5 12: INV6 13: INV7 14: OPG 15: MM
16: VRT 17: PLN 18: PRO1 19: PRO2 20: ROD 21: SYN 22: UNC
23: VIR1 24: VIR2

Database:

genbank97
25: BCT1 26: BCT2 27: BCT3 28: BCT4 29: BCT5 30: BCT6 31: BCT7
32: BCT8 33: BCT9 34: GEN1 35: GEN2 36: HNG 37: INV1 38: INV2
39: INV3 40: INV4 41: INV5 42: INV6 43: INV7 44: INV8 45: INV9
46: MAM1 47: MAM2 48: MAM3 49: VRT1 50: VRT2 51: VRT3 52: PAT1
53: PAT2 54: PAT3 55: PAT4 56: PHG 57: PLN1 58: PLN2 59: PLN3
60: PLN4 61: PLN5 62: PLN6 63: PLN7 64: PLN8 65: PLN9 66: PLN10
67: PRI1 68: PRI2 69: PRI3 70: PRI4 71: PRI5 72: PRI6 73: PRI7
74: PRI8 75: PRI9 76: PRI10 77: PRI11 78: PRI12 79: PRI13
80: PRI14 81: ROD1 82: ROD2 83: ROD3 84: ROD4 85: ROD5 86: ROD6
87: ROD7 88: ROD8 89: STR 90: SYN 91: DNA 92: VRL1 93: VRL2
94: VRL3 95: VRL4 96: VRL5 97: VRL6 98: VRL7 99: VRL8 100: VRL9
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101: BCT 102: GEN 103: INV1 104: INV2 105: MAM 106: VRT
107: PHG 108: PLN 109: PRI1 110: PRI2 111: ROD 112: SYN
113: DNA 114: VRL
u-emb148_97
115: Part1 116: Part2

Database:

Statistics: Mean 11.674; Variance 5.373; scale 2.173

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID Description Pred. No.

1	979	62.5	2100	33	YEPLCR	Yersinia pestis lcrG	0.00e+00
2	951	60.7	981	33	YEPPIVANT	Y.pseudotuberculosis	0.00e+00
3	947	60.5	2201	33	YEPICRGVHP	Yersinia pseudotuberc	0.00e+00
4	903	57.7	975	33	YEP6PVANT	Y.enterocolitica V an	0.00e+00
5	901	57.5	975	33	YE108VANT	Y.enterocolitica V an	0.00e+00
6	899	57.4	975	33	YE527VANT	Y.enterocolitica V an	0.00e+00
7	897	57.3	975	33	YEB08VANT	Y.enterocolitica V an	0.00e+00
8	767	49.0	1002	33	YE314VANT	Y.enterocolitica V an	0.00e+00
9	757	48.3	1002	33	YENCVTANT	Y.enterocolitica V an	0.00e+00
10	516	33.0	5383	33	YPCAF	Y.pseudotuberculosis	0.00e+00
11	212	13.5	240	31	S78727	lcrG operon: lcrV-V	2.42e-154
12	53	3.4	391	74	HSU21500	WT1-W1ms' tumor supp	6.85e-19
13	31	2.0	670	62	RIC51NE12	Human chromosome 17q2	1.02e-03
14	31	2.0	1867	59	DDIPRKT	Rice retroposon P-SIN	1.02e-03
15	31	2.0	7407	76	HUMG1PRD	Dicystotellum discoid	1.02e-03
16	31	2.0	115	87	RNEDNRB7	Human gene for gastr	1.02e-03
17	30	1.9	205	44	PIWTR	Rattus norvegicus end	4.10e-03
18	30	1.9	271	82	MMGM035	Polistes annularis (C	4.10e-03
19	29	1.9	680	66	YSCF0N80	Mouse rearranged V(H)	1.61e-02
20	29	1.9	1800	63	SCPRTF	Yeast (S.cerevisiae)	1.61e-02
21	29	1.9	1813	85	MUSIGHVJ2	S.cerevisiae gene for	4.10e-03
22	30	1.9	1823	85	MUSIGHVY1	Mouse Ig germline H-c	4.10e-03
23	29	1.9	1839	63	SCU12825	Saccharomyces cerevis	4.10e-03
24	30	1.9	1888	57	ATHUBICOF	Arabidopsis thaliana	1.61e-02
25	29	1.9	1920	43	OMMCRTSBI	O.sloanei S-crysalin	1.61e-02
26	29	1.9	2359	49	CPMALPR	C.parvum gene for wal	1.61e-02
27	29	1.9	2363	64	PFARPHR	P.falciparum 240 kDa	1.61e-02
28	29	1.9	2835	64	SCYRL028W	S.cerevisiae chromoso	4.10e-03
29	30	1.9	2855	60	NCU17641	Neurospora crassa vac	1.61e-02
30	29	1.9	3178	44	DMP0INT1A	D.melanogaster mRNA f	4.10e-03
31	30	1.9	3178	44	S66865	pnt-pooled {P1 trans	4.10e-03
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35	30	1.9	7176	44	PRACPSI	Plasmodium falciparum	4.10e-03
36	30	1.9	12805	2	SC128XV	S.cerevisiae 12.8 Kbp	4.10e-03
37	30	1.9	12805	108	SC128XV	S.cerevisiae 12.8 Kbp	4.10e-03
38	30	1.9	25759	87	RNMHC3	Rat embryonic skeleta	4.10e-03
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40	30	1.9	28142	71	HS15886	Human DNA sequence fr	4.10e-03
41	30	1.9	31205	73	CEC06G1	Caenorhabditis elegans	1.61e-02
42	29	1.9	38461	73	HSU165H7	Human DNA sequence fr	4.10e-03
43	30	1.9	39960	110	HSU162C4	Human DNA sequence fr	4.10e-03
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ALIGNMENTS

RESULT 1
LOCUS YEPLCR 2100 bp DNA BCT 27-MAR-1992
DEFINITION Yersinia pestis lcrG, lcrV, and lcrH genes, complete cds.
ACCESSION M26405
KEYWORDS 9155448
SOURCE lcrG protein; lcrH protein; lcrV protein; V antigen.
ORGANISM 75kb virulence plasmid.
Yersinia pestis
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
1 (bases 1 to 2100)
Price,S.B., Leung,K.Y., Barve,S.S. and Straley,S.C.
Molecular analysis of lcrGH, the V antigen operon of Yersinia
pestis
JOURNAL J. Bacteriol. 171, 5646-5653 (1989)
MEDLINE 90008806
COMMENT Computer readable copy of sequence [J. Bacteriol. (1989) In press]
kindly submitted by Price,S.
07-AUG-1989.

FEATURES
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Db	541 gtggacaaccttactgcgtcatggttccttcgaagtttagagaagtgttgctcaagttcaaa 600
OY	646 GTGGACAACACTTACGTGCATCGTGTTCTTCAGGTTTAGAAGAATTCGTCACGTTACTCAA 705
Db	601 gataaaaaatatagatatltccaatataatatgatcccgagaagaagtcggaggttttgc 660
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OY	1006 GATTCAATGAATCATCATCGTGTATGCCCGCTACCAAGTTCGCGAAGAAATTAAGTACGCTT 1065
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DEFINITION		Y.pseudotuberculosis V antigen gene.	
ACCESSION		X96802	
NID		91405834	
KEYWORDS		V antigen.	
SOURCE		Yersinia pseudotuberculosis.	
ORGANISM		Yersinia pseudotuberculosis	
		Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.	
REFERENCE		1 (bases 1 to 981)	
AUTHORS		Roggenkamp, A. and Hoesemann, J.	
TITLE		Contribution of V antigen and anti-V antigen antibodies to an infection with different Yersinia strains	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 981)	
AUTHORS		Roggenkamp, A.	
TITLE		Direct Submission	
JOURNAL		Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG	
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LOCUS DEFINITION Y. enterocolitica V antigen gene, strain Y-96-P.
ACCESSION X96801
NID 91405830
KEYWORDS V antigen.
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SOURCE
ORGANISM
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Yersinia enterocolitica (type 0:9)
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE
1 (bases 1 to 975)
AUTHORS
Roggenkamp, A. and Heesemann, J.
TITLE
Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL
Unpublished
2 (bases 1 to 975)
AUTHORS
Roggenkamp, A.
TITLE
Direct Submission
JOURNAL
Submitted (22-Mar-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
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BASE COUNT 335 a 177 c 194 g 269 t
ORIGIN
Query Match 57.7%; Score 903; DB 33; Length 975;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 936; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
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Db 961 gatgacacg 969
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Qy 1546 gatgacacg 1554

RESULT 5 YE108VANT 975 bp DNA BCT 21-JUN-1996
LOCUS
DEFINITION Y.enterocolitica V antigen gene, strain Y-108-P.
ACCESSION X96799
NID 91405822
KEYWORDS V antigen.
SOURCE Yersinia enterocolitica.
ORGANISM Yersinia enterocolitica.
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Roggenkamp, A. and Heesemann, J.
TITLE Contribution of V antigen and anti-V antigen antibodies to an
JOURNAL infection with different Yersinia strains
REFERENCE 2 (bases 1 to 975)
AUTHORS Roggenkamp, A.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG

FEATURES
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BASE COUNT 341 a 173 c 190 g 271 t

ORIGIN

Query Match 57.5%; Score 901; DB 33; Length 975;
Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 935; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Qy 706 gataaagaatgataatctccatlaaatgataatgataatgataatgataatgataatgata 765
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Qy 1546 gatgacacg 1554

RESULT 6
LOCUS YRS27VANT 975 bp DNA BCT 21-JUN-1996
DEFINITION Y. enterocolitica V antigen gene, serotype 05/27.
ACCESSION X96800
NID g1405826
KEYWORDS V antigen.
SOURCE Yersinia enterocolitica.
ORGANISM Yersinia enterocolitica.
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Roggenkamp, A. and Heesemann, J.
TITLES Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roggenkamp, A.
TITLES Direct Submision
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
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BASE COUNT 339 a 173 c 192 g 271 t
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Best Local Similarity 96.4%; Pred. No. 0.00e+00;
Matches 934; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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Oy 1546 GATGACAGC 1554
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DEFINITION Y. enterocolitica V antigen gene, strain 8081.
ACCESSION X96798
NID g1405828
KEYWORDS V antigen.
SOURCE Yersinia enterocolitica (type 0:8).
ORGANISM Yersinia enterocolitica (type 0:8).
Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
REFERENCE 1 (bases 1 to 975)
AUTHORS Roggenkamp, A. and Heesemann, J.
TITLES Contribution of V antigen and anti-V antigen antibodies to an
infection with different Yersinia strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Roggenkamp, A.
TITLES Direct Submision
JOURNAL Submitted (22-MAR-1996) A. Roggenkamp, Hygiene and Microbiology,
University of Wuerzburg, Josef-Schneider Strasse 2, 97080
Wuerzburg, FRG
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D	b	481	accgcggaattaaagatttatcagttatctaaagccgaattaataagatctgctagt	540
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D	b	601	tatacagatgaaggaattttaaagccagcgacaggtacaaaattctcaagaanaatgcct	660
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D	b	781	aattcgaagattcatatctcttatataaagaataatgaattatctcatcttgcac	840
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D	b	961	tatgattcagtaatgcgaagctctgctagatgaacag	996
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DEFINITION			Y enterocolitica V antigen gene, strain NCTC.	21-JUN-1996
ACCESSION			X6797	
ENTRY			gi405832	
KEYWORDS			V antigen.	
SOURCE			Yersinia enterocolitica (type 0:8).	
ORGANISM			Yersinia enterocolitica; gamma subdivision; Enterobacteriaceae; Yersinia.	
REFERENCE			1 (bases 1 to 1002)	
AUTHORS			Rogenkamp, A. and Heesemann, J.	
TITLE			Contribution of V antigen and anti-V antigen antibodies to an infection with different Yersinia strains	
JOURNAL			Unpublished	
REFERENCE			2 (bases 1 to 1002)	
AUTHORS			Rogenkamp, A.	
TITLE			Direct Submission	
JOURNAL			Submitted (22-MAR-1996) A. Rogenkamp, Hygiene and Microbiology, University of Wuerzburg, Josef-Schneider Strasse 2, 97080 Wuerzburg, FRG	
FEATURES			Location/Qualifiers	
SOURCE			1..1002	

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Plasmid, 240 nt].
ACCESSION S38727
NID 9250552
KEYWORDS
SOURCE Yersinia pseudotuberculosis py995.
ORGANISM Yersinia pseudotuberculosis
REFERENCE 1 (bases 1 to 240)
Molin,V.L., Pokrovskaya,M.S., Telepnev,M.V., Kutyrev,V.V.,
Vidyaeva,N.A., Filipov,A.A. and Smirnov,G.B.
The difference in the lcrV sequences between Y. pestis and Y.
pseudotuberculosis and its application for characterization of Y.
pseudotuberculosis strains
Microb. Pathog. 12 (3), 165-175 (1992)
JOURNAL
MEDLINE
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI glibseq 107284] from the original journal article.
This sequence comes from Fig. 2.
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Matches 226; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Db 181 aagaattctcttgaagtgagaaaaaagaacggcggttgggtatctcgaagactca 240
QY 1294 AAGGACTTCTTGGAAGTGAGAAATTAAGAACCGGGCGTTGGTAACTGAAAAACTCA 1353
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DEFINITION WT1=Wilms' tumor suppressor protein [human, fetal kidney, mRNA, 521
nt].
ACCESSION S75264
NID 9896246
KEYWORDS
SOURCE human fetal kidney.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 521)
AUTHORS Hamilton,T.B., Barilla,K.C. and Romanik,P.J.
TITLE High affinity binding sites for the Wilms' tumour suppressor
protein WT1
Nucleic Acids Res. 23 (2), 277-284 (1995)
JOURNAL
MEDLINE
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI glibseq 160293] from the original journal article.
This sequence comes from Fig. 1A.
COMMENT
FEATURES
Location/Qualifiers
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ORIGIN
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